

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	90.9	29751	12	ADJ39000		Adj39000 SARS CORO
2	16	72.7	619	10	ADK53384		Adk53384 Plant DNA
3	16	72.7	619	10	ADK57664		Adk57664 Plant DNA
4	16	72.7	619	11	ADM45449		Adm45449 Insect re
5	16	72.7	672	10	ADM44886		Adm44886 Insect re
6	16	72.7	686	10	ADK57646		Adk57646 Plant DNA
7	16	72.7	686	10	ADK53332		Adk53332 Plant DNA
8	16	696	11	ADM45452		Adm45452 Insect re	
9	15	68.2	534	6	ABN69216		Abn69216 Streptococ
10	15	68.2	537	8	ACA50276		Aca50276 Prokaryot
c 11	15	68.2	627	6	ABS61473		Abs61473 Prostate
c 12	15	68.2	1101	13	ADR61500		Adr61500 Cotton CD
c 13	15	68.2	1191	5	ABA14473		Aba14473 Human ner
c 14	15	68.2	1191	4	ABA14472		Aba14472 Human ner
c 15	15	68.2	1820	4	AAI22168		Aai22168 Probe #12
c 16	15	68.2	1820	4	ABA67247		Aba67247 Human foe
c 17	15	68.2	1820	4	AAI47467		Aai47467 Probe #16
c 18	15	68.2	1820	4	ABA49335		Aba49335 Human bre
c 19	15	68.2	1820	4	ABA34342		Aba34342 Probe #12
c	15	68.2	1820	4	Aak15686		Aak15686 Human bra
c 21	15	68.2	1820	5	AAI07869		Aai07869 Probe #78
c 22	15	68.2	1820	6	ABS15429		Abs15429 Human gen
c 23	15	68.2	1870	4	AAI21124		Aai21124 Probe #14
c 24	15	68.2	1870	4	ABA67247		Aba67247 Human foe
c 25	15	68.2	1870	4	AAI19420		Aai19420 Probe #15
c 26	15	68.2	1870	4	ABA51239		Aba51239 Human bre
c 27	15	68.2	1870	4	ABA36163		Aba36163 Probe #14
c 28	15	68.2	1870	4	AAK13349		Aak13349 Human bon
c 29	15	68.2	1870	4	AAK17541		Aak17541 Human bra
c 30	15	68.2	1870	6	ABS17430		Abs17430 Human gen
c 31	15	68.2	1966	4	AAI12930		Aai12930 Probe #28
c 32	15	68.2	1966	4	ABA54631		Aba54631 Human foe
c 33	15	68.2	1966	4	AAI34291		Aai34291 Probe #29
c 34	15	68.2	1966	4	ABA44181		Aba44181 Human bre
c 35	15	68.2	1966	4	ABA24415		Aba24415 Probe #28
c 36	15	68.2	1966	4	AAK02920		Aak02920 Human bra
c 37	15	68.2	1966	5	AAI02849		Aai02849 Probe #28
c 38	15	68.2	1966	6	ABS02874		Abs02874 Human gen
c 39	15	68.2	2394	10	ADC137626		Adc137626 Human nuc
c 40	15	68.2	4064	4	ABL01842		Abi01842 Drosophil
c 41	15	68.2	4064	4	ABL03058		Abi03058 Drosophil
c 42	15	68.2	4089	4	ABL04554		Abi04554 Drosophil
c 43	15	68.2	4317	13	ADR14707		Adr14707 Human NF-
c 44	15	68.2	43599	6	ABK84242		Abk84242 Human CDN
c 45	14	63.6	325	2	AAT19998		Aat19998 Human Gen
c 46	14	63.6	348	6	ABN92664		Abn92664 Staphyloc
c 47	14	63.6	348	13	ADS11314		Ado11314 Staphyloc
c 48	14	63.6	534	3	ABN6215		Abn6215 Streptoco
c 49	14	63.6	1240	3	AAC3227		Aac3227 Arabidops
c 50	14	63.6	1278	13	ADT45310		Adt45310 Bacterial
c 51	14	63.6	1341	4	AAF28159		Aaf28159 Rice cent
c 52	14	63.6	1860	13	ADDS16556		Ades16556 B. hensel
c 53	14	63.6	2350	10	ADES5033		Ades5033 Rat gene
c 54	14	63.6	2350	10	ADE55037		Ades55037 Rat gene
c 55	14	63.6	2457	10	ACF70597		Act70597 Photonhab
c 56	14	63.6	3170	4	AAH54485		Aah54485 S. epider
c 57	14	63.6	3504	10	ADB95029		Adb95029 S. neofor
c 58	14	63.6	4314	8	ACA46888		Aca46888 Prokaryot
c 59	14	63.6	4323	5	AAS79450		Aas79450 DNA encod
c 60	14	63.6	4329	4	AAH5329		Aah5329 S. epider
c 61	14	63.6	9342	4	ABL02454		Abi02454 Drosophil
c 62	14	63.6	18895	13	ADS16655		Adi16655 B. hensel
c 63	14	63.6	47493	9	ADA02549		Ada02549 Mouse Wnt
c 64	14	63.6	47493	10	ADB72287		Adb72287 Mouse Wnt
c 65	14	63.6	47493	10	ADEB5797		Ades5797 Mouse Wnt
c 66	14	63.6	76180	13	ABD13385		Abd13385 Human can
c 67	14	63.6	76698	12	ADU84182		Adi84182 Human c-r
c 68	14	63.6	110000	4	AAI99682_07		Continuation (8 of 8)
c 69	14	63.6	110000	6	ABN71527		Abn71527 Streptoco
c 70	14	63.6	110000	6	ABNT1527_00		Continuation (41 of 41)
c 71	14	63.6	110000	10	ACF67367_40		Continuation (8 of 8)
c 72	14	63.6	110000	10	ACF65388_07		Continuation (8 of 8)
c 73	14	63.6	190000	10	ADU13752		Adu13752 Ostearco
c 74	14	63.6	247544	12	ADQ59419		Adq59419 Human can
c 75	13	59.1	21	6	ABA04625		Abi04625 MOL3 reve
c 76	13	59.1	21	10	ADU87878		Adu87878 G-coupled
c 77	13	59.1	21	12	ADN38524		Adn38524 Novel_hum
c 78	13	59.1	190	2	AAQ76533		Aaq76533 Human gen
c 79	13	59.1	200	12	ACB189259		Acb189259 Human gen
c 80	13	59.1	240	11	ACH94421		Ach94421 Klebsiell
c 81	13	59.1	304	10	ADC72386		Adc72386 DNA Seq_I
c 82	13	59.1	305	6	ABV88798		Abv88798 Human col
c 83	13	59.1	319	6	ABN19496		Abn19496 Human ORF
c 84	13	59.1	413	12	ADP5241		Adp5241 Cotton ex
c 85	13	59.1	438	3	AAA82241		Aaa82241 N. mening
c 86	13	59.1	445	6	ABV97902		Abv97902 Human pan
c 87	13	59.1	478	4	ABA57952		Aba57952 Human foe
c 88	13	59.1	478	4	AAI37549		Aai37549 Probe #62
c 89	13	59.1	478	4	Aak131673		Aak131673 Human bon
c 90	13	59.1	478	4	AAK06027		Aak06027 Human bra
c 91	13	59.1	478	4	ABS11357		Abs11357 Human liv
c 92	13	59.1	478	6	ABS016429		Abs016429 Human gen
c 93	13	59.1	486	9	ACH20490		Ach20490 Human adu

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

\$

Result No.	Score	Query	Match	Length	DB	ID
1	20	90.9	29751	12	ADJ39000	SARS CORO
2	16	72.7	619	10	ADK53384	Plant DNA
3	16	72.7	619	10	ADK57664	Plant DNA
4	16	72.7	619	11	ADM45449	Insect re
5	16	72.7	672	10	ADM44886	Insect re
6	16	72.7	686	10	ADK57646	Plant DNA
7	16	72.7	686	10	ADK53332	Plant DNA
8	16	72.7	696	11	ADM45452	Insect re
9	15	68.2	534	6	ABN69216	Streptococ
10	15	68.2	537	8	ACA50276	Prokaryot
c 11	15	68.2	627	6	ABS61473	Prostate
c 12	15	68.2	1101	13	ADR61500	Cotton CD
c 13	15	68.2	1191	5	ABA14473	Human ner
c 14	15	68.2	1191	4	ABA14472	Human ner
c 15	15	68.2	1820	4	AAI22168	Probe #12
c 16	15	68.2	1820	4	ABA67247	Human foe
c 17	15	68.2	1820	4	AAI47467	Probe #16
c 18	15	68.2	1820	4	ABA49335	Human bre
c 19	15	68.2	1820	4	ABA34342	Probe #12
c	15	68.2	1820	4	Aak15686	Human bra

c 94	13	59.1	AAK91848	Human cDN	Aav90767 Nucleotid
c 95	13	59.1	AAK9253	Human cDN	Abv20603 Aspergill
c 96	13	59.1	ADL28275	Adl28275 5' end of	Abt18787 Aspergill
c 97	13	59.1	539	Adl29680 5' end of	Adr03843 Carotenoi
c 98	13	59.1	539	Ach75524 Human gen	Adr03923 Marshid of
c 99	13	59.1	570	Ach75524 Human gen	Abt13067 Arabidops
c 100	13	59.1	584	Aac35392 Arabidops	Ad68438 Arabidops
c 101	13	59.1	585	ABZ13833 Arabidops	Aav90893 Nucleotid
c 102	13	59.1	603	ADK6004 Plant DNA	Aav90893 Nucleotid
c 103	13	59.1	625	ABV96002 Human pan	Aak94748 Human ful
c 104	13	59.1	646	ABV96049 Human pan	Adl13185 Full leng
c 105	13	59.1	678	AAS5311 Human pan	Adq23265 Human sof
c 106	13	59.1	816	AAC34154 Prokaryot	Adr03735 Full leng
c 107	13	59.1	709	ADK56318 Plant DNA	Aat97609 Human EA
c 108	13	59.1	714	ACD2613 Human col	Aca2424 Prokaryot
c 109	13	59.1	796	ABN9064 Arabidops	Adr85477 Aspergill
c 110	13	59.1	797	AAA78471 Plant SDF	Aab89905 Human bon
c 111	13	59.1	816	AAT6162 H. pylori	Abk43659 Human encod
c 112	13	59.1	816	AAX30429 H. pylori	Adi54046 cDNA enco
c 113	13	59.1	816	AAS53726 Helicobac	Adr84890 Aspergill
c 114	13	59.1	816	AAS53890 Helicobac	Abz35234 Human gen
c 115	13	59.1	816	Aca34980 Prokaryot	Adr79065 Human pro
c 116	13	59.1	833	ACCA3927 Nucleotid	Adr54610 Human ova
c 117	13	59.1	840	AAT6162 H. pylori	Abz13871 Human oval
c 118	13	59.1	855	ABV30274 Human pro	Adm24122 Human PRO
c 119	13	59.1	885	AAC77620 Human can	Acr38620 Tumour-as
c 120	13	59.1	916	AAH65497 C. glutamici	Abt1210 Aspergill
c 121	13	59.1	944	ABK65152 Arabidops	Abz78236 A. niger
c 122	13	59.1	947	ADG16634 Thalecres	Adr05424 Aspergill
c 123	13	59.1	947	ADD30295 Plant Yie	Ach03928 Human cDN
c 124	13	59.1	947	ADG1550 Plant tra	Acc50076 Coding se
c 125	13	59.1	954	AAH65497 Prokaryot	Acc50076 Breast ca
c 126	13	59.1	1024	ABX65613 Helicobac	Adr90653 Human hep
c 127	13	59.1	1026	AAI81237 Human pol	Adr90653 Human pro
c 128	13	59.1	1065	AAST0168 DNA encod	Adq86121 Human cum
c 129	13	59.1	1137	ADS49156 Bacterial	Acn38620
c 130	13	59.1	1140	AAC5746 Human sec	Adr79067 Human pro
c 131	13	59.1	1146	AAC44595 Prokaryot	Adr85339 Aspergill
c 132	13	59.1	1161	ADP03576 Bacterial	Abt18193 Aspergill
c 133	13	59.1	1387	ADG30625 Plant Yie	Abz34770 Coding se
c 134	13	59.1	1387	ADG1852 Plant tra	Acc50076
c 135	13	59.1	1411	ADG2988 Transcript	Acc50076
c 136	13	59.1	1411	ABN97326 Gene #382	Acc50076
c 137	13	59.1	1411	ADQ86272 Human tum	Adr44022 Human col
c 138	13	59.1	1419	ADG7442 Human tum	Adr8532 Aspergill
c 139	13	59.1	1422	ADQ5933 T cell ac	Adr8532 Aspergill
c 140	13	59.1	1476	AAI63051 Human pol	Adr8532 Aspergill
c 141	13	59.1	1539	ABD21639 Thogoto v	Adr8532 Aspergill
c 142	13	59.1	1546	AAI58565 Human pol	Adr84665 Aspergill
c 143	13	59.1	1546	ADQ98782 DNA encod	Aat85096 Nucleotid
c 144	13	59.1	1546	ADQ98782 Novel hum	Abd110750 Droophil
c 145	13	59.1	1583	AAAC40650 Arabidops	Adr84303 Aspergill
c 146	13	59.1	1583	AAI63946 Human pol	Abd13738 Droophil
c 147	13	59.1	1584	AAAS31613 cDNA enco	Adr03946 Carotenoi
c 148	13	59.1	1584	ABK43947 DNA encod	Adr03946 Genetical
c 149	13	59.1	1584	ADG24497 Human PRO	Adr03946 Genetical
c 150	13	59.1	1584	ADDB48542 Novel hum	Adr03946 Genetical
c 151	13	59.1	1584	AAI63946 Human pol	Adr03946 Genetical
c 152	13	59.1	1639	ADA73069 Rice gene	Adr03946 Genetical
c 153	13	59.1	1683	ADEB1196 Orf12 cod	Adr03946 Genetical
c 154	13	59.1	1739	ADG12509 Plant tra	Adr03946 Genetical
c 155	13	59.1	1767	ABT21218 Aspergill	Adr03946 Genetical
c 156	13	59.1	1775	ADG42510 Plant tra	Adr03946 Genetical
c 157	13	59.1	1778	ADBS4775 Primary r	Adr03946 Genetical
c 158	13	59.1	1791	ADT19398 Aspergill	Adr03946 Genetical
c 159	13	59.1	1830	ABK43948 Human nov	Adr03946 Genetical
c 160	13	59.1	1854	ABT18804 Aspergill	Adr03946 Genetical
c 161	13	59.1	1867	ABT20620 Aspergill	Adr03946 Genetical
c 162	13	59.1	2000	ADA73355 Rice gene	Adr03946 Genetical
c 163	13	59.1	2025	ABT15381 Aspergill	Adr03946 Genetical
c 164	13	59.1	2047	ABT21201 Aspergill	Adr03946 Genetical
c 165	13	59.1	2047	ABL93809 Human sec	Adr03946 Genetical
c 166	13	59.1	2047	ABX62972 Human act	Adr03946 Genetical
c 167	13	59.1	2077	AAV90767	Adr03946 Genetical
c 168	13	59.1	2105	ABT18787 Aspergill	Adr03946 Genetical
c 169	13	59.1	2105	ABT18787 Aspergill	Adr03946 Genetical
c 170	13	59.1	2160	ADR03843 Carotenoi	Adr03946 Genetical
c 171	13	59.1	2160	ADR03843 Carotenoi	Adr03946 Genetical
c 172	13	59.1	2418	ABZ13067 Arabidops	Adr03946 Genetical
c 173	13	59.1	2418	ADA68438 Arabidops	Adr03946 Genetical
c 174	13	59.1	2466	AAV90769 Human ful	Adr03946 Genetical
c 175	13	59.1	2518	AAK94748 Human ful	Adr03946 Genetical
c 176	13	59.1	2518	Adl13185 Full leng	Adr03946 Genetical
c 177	13	59.1	2555	ADQ23265 Human sof	Adr03946 Genetical
c 178	13	59.1	2555	Adr03735 Full leng	Adr03946 Genetical
c 179	13	59.1	2571	AAT97609 Human EA	Adr03946 Genetical
c 180	13	59.1	2892	ACA4242 Prokaryot	Adr03946 Genetical
c 181	13	59.1	2916	Adr85477 Aspergill	Adr03946 Genetical
c 182	13	59.1	2933	AAB89905 Human ova	Adr03946 Genetical
c 183	13	59.1	2991	ABK43659 Human encod	Adr03946 Genetical
c 184	13	59.1	2991	Adi54046 cDNA enco	Adr03946 Genetical
c 185	13	59.1	3085	Adr84890 Aspergill	Adr03946 Genetical
c 186	13	59.1	3170	ABZ25234 Human gen	Adr03946 Genetical
c 187	13	59.1	3273	Adr20024 Aspergill	Adr03946 Genetical
c 188	13	59.1	3523	ABO54610 Human pro	Adr03946 Genetical
c 189	13	59.1	3849	AAI63871 Human PRO	Adr03946 Genetical
c 190	13	59.1	3849	ADM24422 Human PRO	Adr03946 Genetical
c 191	13	59.1	3854	AACT97610 Human E2A	Adr03946 Genetical
c 192	13	59.1	3854	ABT181810 Human E2A	Adr03946 Genetical
c 193	13	59.1	3867	ABT20024 Aspergill	Adr03946 Genetical
c 194	13	59.1	3872	ABD79063 Human pro	Adr03946 Genetical
c 195	13	59.1	3914	ADOB8121 Human cum	Adr03946 Genetical
c 196	13	59.1	3914	ACN38620	Adr03946 Genetical
c 197	13	59.1	3916	ABZ78236 A. niger	Adr03946 Genetical
c 198	13	59.1	3919	ADT05424 Aspergill	Adr03946 Genetical
c 199	13	59.1	3922	ACH03928 Human cDN	Adr03946 Genetical
c 200	13	59.1	3935	ABZ34770 Coding se	Adr03946 Genetical
c 201	13	59.1	3935	ACC50076 Breast ca	Adr03946 Genetical
c 202	13	59.1	3935	ADP90653 Human hep	Adr03946 Genetical
c 203	13	59.1	3935	ADP90653 Human pro	Adr03946 Genetical
c 204	13	59.1	4025	ADP79067 Human PRO	Adr03946 Genetical
c 205	13	59.1	4033	ADP79067 Human PRO	Adr03946 Genetical
c 206	13	59.1	4105	ABT18193 Aspergill	Adr03946 Genetical
c 207	13	59.1	4125	ABD44022 Human col	Adr03946 Genetical
c 208	13	59.1	4657	ADR85252 Aspergill	Adr03946 Genetical
c 209	13	59.1	4657	ABA04591 MOL3 codi	Adr03946 Genetical
c 210	13	59.1	4894	ADJ879067 Human PRO	Adr03946 Genetical
c 211	13	59.1	5195	ADP59868 Human con	Adr03946 Genetical
c 212	13	59.1	5733	AAK95416 Aspergill	Adr03946 Genetical
c 213	13	59.1	5869	ADB10476 Droophil	Adr03946 Genetical
c 214	13	59.1	6373	ABD10476 Droophil	Adr03946 Genetical
c 215	13	59.1	6657	ADR84665 Aspergill	Adr03946 Genetical
c 216	13	59.1	7581	AAPF5096 Nucleotid	Adr03946 Genetical
c 217	13	59.1	7811	ABD10750 Droophil	Adr03946 Genetical
c 218	13	59.1	9085	ABD15805 Aspergill	Adr03946 Genetical
c 219	13	59.1	10303	ABU13738 Drosophil	Adr03946 Genetical
c 220	13	59.1	11611	ABD10476 Droophil	Adr03946 Genetical
c 221	13	59.1	11611	ADP03926	Adr03946 Genetical
c 222	13	59.1	13160	ABA15804 Human ner	Adr03946 Genetical
c 223	13	59.1	13160	ADW20183 Alternati	Adr03946 Genetical
c 224	13	59.1	13189	ABA15805 Human ner	Adr03946 Genetical
c 225	13	59.1	13189	ADM20184 Alternati	Adr03946 Genetical
c 226	13	59.1	15739	ABD10476 Droophil	Adr03946 Genetical
c 227	13	59.1	15739	ADP03926	Adr03946 Genetical
c 228	13	59.1	16103	ABA15804 Human ner	Adr03946 Genetical
c 229	13	59.1	16103	ADP03926	Adr03946 Genetical
c 230	13	59.1	16103	ABA15805 Aspergill	Adr03946 Genetical
c 231	13	59.1	16245	ABD10476 Droophil	Adr03946 Genetical
c 232	13	59.1	16245	ADP03926	Adr03946 Genetical
c 233	13	59.1	16954	ABA15804 Human ner	Adr03946 Genetical
c 234	13	59.1	16954	ADP03926	Adr03946 Genetical
c 235	13	59.1	16954	ABA15805 Aspergill	Adr03946 Genetical
c 236	13	59.1	16954	ABD10476 Droophil	Adr03946 Genetical
c 237	13	59.1	17118	ABA15804 Human ner	Adr03946 Genetical
c 238	13	59.1	17118	ABT15381 Aspergill	Adr03946 Genetical
c 239	13	59.1	17238	ABX62972 Human act	Adr03946 Genetical

240	13	59.1	17238	13	ADRO3880	Carceno	XX	SARS coronavirus nucleotide sequence.
241	13	59.1	17238	13	ADRO3961	Genetical	DE	
242	13	59.1	17238	13	ADRO3960	Genetical	XX	
243	13	59.1	17593	13	ADRO3884	Carceno	KW	small interfering RNA; siRNA; modified ribonucleotide; viral replication inhibition; hepatitis C virus; HCV; hepatitis C; antiinflammatory; hepatotropic; virucide; hepatitis A virus; hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus; rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus; metapneumovirus; coronavirus; viral infection; gene; ds.
244	13	59.1	17593	13	ADRO3964	Genetical	KW	
245	13	59.1	17756	13	ADRO3889	Carceno	KW	
246	13	59.1	17756	13	ADRO3969	Genetical	KW	
247	13	59.1	17877	13	ADRO3879	Carceno	KW	
248	13	59.1	17877	13	ADRO3959	Genetical	KW	
249	13	59.1	18333	13	ADRO3893	Carceno	XX	SARS coronavirus.
250	13	59.1	18333	13	ADRO3973	Genetical	OS	
251	13	59.1	18449	13	ADRO3892	Carceno	XX	
252	13	59.1	18449	13	ADRO3891	Carceno	PN	WO2004011647-A1.
253	13	59.1	18449	13	ADRO3883	Carceno	XX	
254	13	59.1	18449	13	ADRO3962	Genetical	PD	05-FEB-2004.
255	13	59.1	18449	13	ADRO3963	Genetical	XX	25-JUL-2003; 2003WO-US023104.
256	13	59.1	18449	13	ADRO3973	Genetical	PF	
257	13	59.1	18617	13	ADRO3892	Carceno	XX	
258	13	59.1	18617	13	ADRO3972	Genetical	PR	26-JUL-2002; 2002US-0398605P.
259	13	59.1	19491	13	ADRO3887	Carceno	XX	
260	13	59.1	19491	13	ADRO3967	Genetical	PA	(CHIR ) CHIRON CORP.
261	13	59.1	21300	13	ADRO3888	Carceno	XX	
262	13	59.1	21300	13	ADRO3968	Genetical	PI	Han J, Seo MY, Houghton M;
263	13	59.1	23118	4	AAK71708	Human imm	XX	
264	13	59.1	23171	11	ACN44326	Human gen	DR	WPI; 2004-143862/14.
265	13	59.1	27571	12	ADQ59500	Human can	XX	
c 266	13	59.1	29598	2	AAV49554	Human SC2	PT	New RNase resistant small interfering RNA, useful for treating viral infections, e.g., hepatitis C, influenza virus or coronavirus infection.
c 267	13	59.1	32349	4	ABL15430	Drosophil	XX	
c 268	13	59.1	52312	13	ABD3555	Murine ca	XX	Example 10; Fig 3; 74pp. English.
c 269	13	59.1	59767	13	ABD3205	Absc32905	PS	New RNase resistant small interfering RNA (siRNA) which comprises a modified ribonucleotide, where the siRNA is resistant to
c 270	13	59.1	68750	3	AAZ55887	Sorangium	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
c 271	13	59.1	72149	10	ADEB1173	ML-336B 8	CC	comprising a DNA segment encoding the RNA molecule (6),
c 272	13	59.1	95814	13	ADT05644	Haemophil	CC	comprising the vector of (6); (7) inhibiting replication of HCV in cells
c 273	13	59.1	9823	10	ADL13497	Osteoarthr	CC	described: (1) inactivating a virus in a patient; (2) making a modified
c 274	13	59.1	94618	3	AAF22285	BAC conta	CC	siRNA that targets a nucleic acid sequence in a virus; (3) double-
c 275	13	59.1	96593	9	ADA0260	Human RUN	CC	stranded RNA molecule of 10-30 nucleotides that inhibits replication of
c 276	13	59.1	96593	10	ADB7338	Human RUN	CC	hepatitis C virus (HCV); (4) inducing targeted RNA interference toward
c 277	13	59.1	96593	10	AdB95848	Human RUN	CC	target HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector
c 278	13	59.1	96599	9	Ada02981	Mouse Map	CC	comprising a DNA segment encoding the RNA molecule (6),
c 279	13	59.1	96599	10	ADB7219	Cancer	CC	comprising the vector of (6); (7) inhibiting replication of HCV in cells
c 280	13	59.1	96599	10	ADC622751	Mouse Map	CC	carrying HCV; (9) treating hepatitis C in a subject; (10) modified
c 281	13	59.1	96599	12	ADM74576	Murine ca	CC	modified RNA molecules are useful for inactivating virus in mammalian
c 282	13	59.1	110000	2	AAAT42063	Continuation	CC	cells. The siRNAs are useful for treating hepatitis C virus, influenza
c 283	13	59.1	110000	11	ACN44326	Contamination	CC	virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza
c 284	13	59.1	174424	6	ABL68122	Ab188122 Ovary can	CC	virus, rotavirus, reovirus, retrovirus, poliovirus, human Papilloma
c 285	13	59.1	177380	8	ACF622751	Actf67751	CC	viruses, metapneumovirus or coronavirus infections. The methods of the
c 286	13	59.1	177380	10	ADB20870	Mouse can	CC	invention can be used to correct or compensate for cellular physiological
c 287	13	59.1	177380	10	ADB87959	Human UGT	CC	abnormalities involved in conferring susceptibility to viral infections
c 288	13	59.1	177380	10	ADB96342	Human MDR	CC	in patients and/or alleviate symptoms of a viral infection in patients.
c 289	13	59.1	177380	10	ADB22133	Human MDR	CC	The present sequence represents the SARS coronavirus nucleotide sequence,
c 290	13	59.1	181343	12	ADQ19573	Human sof	CC	which is used in an example from the present invention.
c 291	13	59.1	199868	12	ADQ97831	Mouse can	CC	
c 292	13	59.1	203654	10	ABX16034	Absc16034	CC	
c 293	13	59.1	209484	11	ACN44326	Human gen	CC	
c 294	13	59.1	220224	11	ACN44302	Acn44302	CC	
c 295	13	59.1	220803	13	ABD32730	Human can	CC	
c 296	13	59.1	234980	5	AAH68525	C Glutami	CC	
c 297	12	54.5	25	9	ACK27997	Ack27997	XX	Sequence 29751 BP; 8478 A; 5941 C; 6188 G; 9144 T; 0 U; 0 Other;
c 298	12	54.5	25	9	ACI79106	Ac179106	XX	Query Match 90.9%; Score 20; DB 12; Length 29751;
c 299	12	54.5	25	9	ACI12036	Ac112036	XX	Best Local Similarity 75.0%; Pred. No. 0.033%; Matches 5; Mismatches 0; Indels 0; Gaps 0;
c 300	12	54.5	27	2	AAX80816	A.thalian	XX	RESULT 1 ADJ39000 standard; DNA; 29751 BP. ID ADJ39000; XX AC ADJ39000; ID ADK58384 standard; DNA; 619 BP. DT 06-MAY-2004 (first entry)

## ALIGNMENTS

Qy 1 GUGAACUCACUCGUAGGCU 20  
|:||||:||:||:||:||:||:||:||:||:  
Db 776 GTGAACTACTCGAGTC 795

RESULT 2  
ADK58384  
ID ADK58384  
XX



OS Unidentified.  
 XX WO2003020025-A2.  
 PN 13-MAR-2003.  
 XX 30-AUG-2002; 2002WO-US027882.  
 PF 31-AUG-2001; 2001US-0316319P.  
 PR (DOWC ) DOW CHEM CO.  
 PI Shukla V, Meade T, Larrinu I;  
 XX WPI; 2003-290133/28.  
 XX New isolated nucleic acid having expression that results in an insect resistant phenotype, useful for conferring insect resistance and for producing insect-resistant plants.  
 PS Claim 1; SEQ ID NO 856; 396pp; English.  
 XX This invention relates to a novel isolated nucleic acid comprising, or hybridising under low stringent conditions to, any of the 1214 nucleic acid sequences given in the specification, where the expression of the nucleic acid in a plant results in an insect resistant phenotype. The invention may be useful as a plant protectant or for gene therapy. The genes are derived from *Arabidopsis thaliana*, *Nicotiana benthamiana*, *Oryza sativa* and *Papaver rhoes*. The isolated nucleic acid and vector are useful for conferring insect resistance and for producing insect-resistant plants. The present sequence is that of a DNA sequence of the invention which may confer insect resistance to plants.  
 XX Sequence 619 BP; 133 A; 177 C; 126 T; 0 U; 0 Other;  
 Query Match 72.7%; Score 16; DB 11; Length 619;  
 Best Local Similarity 75.0%; Pred. No. 7.4%;  
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 CUCACUTCGAGCTT 21  
 AC :|||:|||:|||:|||:  
 Db 619 CTCACTCGAGCTT 634

RESULT 6  
 ADK57646 ID ADK57646 Standard; DNA; 686 BP.  
 XX ADK57646;  
 AC XX  
 DT 06-MAY-2004 (first entry)  
 DE Plant DNA sequence which confers altered metabolic characteristic #5029.  
 XX  
 KW altered metabolic characteristic; plant; acid metabolism;  
 KW alcohol metabolism; fatty acid metabolism; alkaloid metabolism;  
 KW branched fatty acid metabolism; ester metabolism; glyceride metabolism;  
 KW amino acid metabolism; carbohydrate metabolism; sterol metabolism;  
 KW phenolic metabolism; carboxylic acid metabolism; terpene metabolism;  
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds-  
 XX Unidentified.  
 OS XX  
 PN WO2003020936-A1.  
 XX DR 2003-313091/30.

DE Insect resistance associated DNA sequence SeqID293.  
 XX 13-MAR-2003.  
 XX insect resistant phenotype; plant protectant; gene therapy;  
 KW *Arabidopsis thaliana*; *Nicotiana benthamiana*; *Oryza sativa*;  
 KW *Papaver rhoes*; rice; insect resistance; insect-resistant plant; ds-  
 XX Unidentified.  
 OS XX  
 PN WO2003020025-A2.  
 XX 13-MAR-2003.  
 PD 03-JUN-2004 (first entry)  
 XX DE Insect resistance associated DNA sequence SeqID293.  
 XX 30-AUG-2002; 2002WO-US027882.  
 XX 31-AUG-2001; 2001US-0316319P.  
 PF (DOWC ) DOW CHEM CO.  
 PI Shukla V, Meade T, Larrinu I;  
 XX WPI; 2003-290133/28.  
 XX Novel genes that confer altered metabolic characteristics in *Nicotiana benthamiana* plants, useful for altering the levels of metabolites e.g. PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
 PR PI  
 XX PS Claim 1; SEQ ID NO 5029; 2576pp; English.  
 XX CC The invention comprises DNA sequences which confer an altered metabolic



Db 622 CTCACCTGAGCTCT 637

RESULT 9  
 ABN6216 standard; DNA; 534 BP.  
 ID ABN6216  
 XX DT 01-JUN-2002 (first entry)  
 DE Streptococcus polynucleotide SBQ ID NO 6345.  
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW Group A streptococcus; Streptococcus pyogenes; antibacterial; gene;  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy; ds;  
 XX Streptococcus pyogenes.  
 OS PN WO200234771-A2.  
 XX PD 02-MAY-2002.  
 XX PP 29-OCT-2001; 2001WO-GB004789.  
 XX PR 27-OCT-2000; 2000GB-00026333.  
 PR 24-NOV-2000; 2000GB-00028727.  
 PR 07-MAR-2001; 2001GB-00005640.  
 XX (CHFR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX PI Telford J, Massignani V, Margarit Y Rossi, Grandi G, Fraser C;  
 PI Tettelin H,  
 XX WPI; 2002-352536/38.  
 DR P-PSDB; ABP28585.  
 XX New Streptococcus protein for the treatment or prevention of infection or  
 PT disease caused by Streptococcus bacteria, such as meningitis, and for  
 PT detecting a compound that binds to the protein.  
 XX Claim 7; Page 3799; 4525PP; English.  
 PS The invention relates to a protein (ABP05413-ABP0895) from group B  
 CC streptococcus (GBS) (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (1) nucleic acids encoding (1), ABN65044-ABN71526 and  
 CC antibodies that bind (1) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a  
 CC biological sample. (1) is used to determine whether a compound binds to  
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (1) may be used to recombinantly produce (1) and may be  
 CC used in gene therapy. Antibodies to (1) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins  
 XX Sequence 534 BP; 186 A; 101 C; 109 G; 138 T; 0 U; 0 Other;  
 Query Match 68.2%; Score 15; DB 6; Length 534;  
 Best Local Similarity 80.0%; Pred. No. 29;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GAACUCUCCUGAG 17  
 Db 94 GAACTCACTCGTGAG 108

XX Sequence 537 BP; 188 A; 101 C; 109 G; 139 T; 0 U; 0 Other;  
 SQ Query Match 68.2%; Score 15; DB 8; Length 537;  
 Best Local Similarity 80.0%; Pred. No 29;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAAUCACUGUGAG 17  
 Db 94 GRACTCACTCGTGAG 108

RESULT 11  
 ABS1473\_C  
 ID ABS1473 standard; cDNA: 627 BP.  
 XX DT 05-NOV-2002 (first entry)  
 AC Prostate specific nucleic acid DEX0259\_81.  
 XX Human; ss; prostate specific nucleic acid; PSNA; prostate cancer;  
 KW cytosolic; non-cancerous prostate disease; PSP; vaccine;  
 KW prostate specific protein; metastasis  
 OS Homo sapiens.  
 XX WO200242776-A2.  
 XX PD 30-MAY-2002.  
 XX PF 01-NOV-2001; 2001WO-US045654.  
 XX PR 01-NOV-2000; 2000US-0244782P.  
 XX PA (DIAD-) DIADEXUS INC.  
 PI Sun Y, Recipon H, Chen S, Liu C;  
 XX DR WPI; 2002-490217/52.  
 XX PT New polypeptide useful for diagnosing and monitoring the presence and  
 PT metastases of prostate cancer in a patient and as a component in  
 PT databases for search analysis as well as in sequence analysis algorithms.  
 XX PS Claim 1; Page 183-184; 242pp; English.

The invention relates to an isolated polypeptide comprising a sequence with 60% identity to one of prostate specific protein (PSP) sequences, or comprising an amino acid sequence encoded by one of 136 nucleotide sequences specific nucleic acids sequences, PSNA, (or a sequence that hybridises to it or is 60% identical to it), given in the specification. Also included are a vector comprising the polynucleotide, a host cell comprising the vector an antibody specific for the PSP proteins and a vaccine comprising the protein or polynucleotide. The PSP and PSNA are useful for detecting the presence and metastases of prostate cancer in a patient. The PSNA is useful for determining the presence of prostate specific protein in a sample, and for treating a patient with prostate cancer, which induces an immune response against the prostate cancer cell expressing the nucleic acid or polypeptide and a kit useful for detecting a risk of cancer or presence of cancer in a patient. PSNA is useful as hybridisation probes to detect, characterise and quantify hybridising nucleic acids from both genomic and transcript-derived nucleic acid samples and also in microarrays. Sequences of PSP and PSNA are useful as components in databases for search analysis as well as in sequence analysis algorithms. PSNA is useful to drive in vivo expression of PSP. The present sequence is a PSNA of the invention

XX Sequence 627 BP; 129 A; 152 C; 169 G; 177 T; 0 U; 0 Other;  
 SQ Query Match 68.2%; Score 15; DB 6; Length 627;

Best Local Similarity 80.0%; Pred. No 29;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAAUCACUGUGAG 17  
 Db 224 GRACTCACTCGTGAG 210

RESULT 12  
 ADR61500 standard; cDNA; 1101 BP.  
 XX ID ADR61500;  
 AC AC  
 XX DT 02-DEC-2004 (first entry)  
 DB Cotton cDNA sequence, SEQ ID 2281.  
 XX KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;  
 KW drought tolerance; plant disease resistance; galactomannan; lignin;  
 KW plant growth regulator; heat tolerance; herbicide tolerance;  
 KW homologous recombination; extreme osmotic condition tolerance;  
 KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;  
 KW stress resistance.  
 XX OS Gossypium hirsutum.  
 XX PN US2004181830-A1.  
 XX PD 16-SEP-2004.  
 XX PP 29-JAN-2004; 2004US-00767795.  
 XX PR 07-MAY-2001; 2001US-00849529.  
 XX PR 12-DEC-2001; 2001US-00021323.  
 XX PA (KOVALIC) KOVALIC D K.  
 PA (ZHOU) ZHOU Y.  
 PA (CAO) CAO Y.  
 XX PI KOVALIC DK, Zhou Y, Cao Y;  
 XX DR WPI; 2004-667718/65.  
 XX PT New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).  
 XX PT Claim 1; SEQ ID NO 2281; 14pp; English.  
 XX PS The invention relates to a recombinant polynucleotide comprising any of the 58758 Cotton plant cDNA sequences mentioned in the specification. Also a recombinant polypeptide comprising any of the 58758 amino acid sequences mentioned in the specification and producing a plant having an improved property. Producing a plant having an improved property comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide comprising a coding sequence for a polypeptide associated with the property, and growing the transformed plant. The polypeptide is useful for improving plant cold tolerance, manipulating growth rate in plant cells by modification of the cell cycle pathway, improving plant drought tolerance, providing increased resistance to plant disease, producing galactomannan (or lignin or plant growth regulators), improving plant heat tolerance, improving plant tolerance to herbicides, increasing the rate of homologous recombination in plants, improving plant tolerance to extreme osmotic conditions or to pathogens or pests, improving yield by modification of photosynthesis, modifying seed oil or protein yield and/or content, improving yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, or improving yield by providing improved plant growth and development under at least one stress condition. The polynucleotide and polypeptide may also be used in recombinant DNA constructs, in physical arrays of molecules, as plant breeding markers, or in computer-based storage and analysis systems. The present sequence

CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from USPTO at CC seqdata.uspto.gov/sequence.html?DocID=20040181830 . However only 6585 CC polynucleotide sequences were available, the remaining 52213 CC polynucleotides and all 58798 protein sequences were not present.

XX Sequence 1101 BP; 308 A; 201 C; 254 G; 338 T; 0 U; 0 Other;

Score 15 ; DB 13; Length 1101;  
Best Local Similarity 73.3%; Pred. No. 29;  
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUGGAGCUC 20  
| :| :| :| :| :| :|  
Db 1027 CTCACTCGTGA GCTC 1041

## RESULT 13

ID ABA14473 standard; DNA; 1191 BP.  
XX ABA14473 ;

DT 23-JAN-2002 (first entry)

XX Human nervous system related polynucleotide SEQ ID NO 6804 .

XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnearily; anti-parkinsonian; antischikling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; anticonvulsant; antifungal; antiparasitic; cariant; immune disorder; cardiovascular disorder; KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds . XX OS Homo sapiens . XX PN WO200159063-A2 . XX PD 16-AUG-2001 . XX PP 17-JAN-2001; 2001WO-US001334 .

XX PR 31-JAN-2000; 2000US-0179065P .

PR 04- FEB-2000; 2000US-0180628P .

PR 24-FEB-2000; 2000US-01B4664P .

PR 02-MAR-2000; 2000US-018635P .

PR 16-MAR-2000; 2000US-0189874P .

PR 17-MAR-2000; 2000US-0190076P .

PR 18-APR-2000; 2000US-019812P .

PR 19-NAY-2000; 2000US-0205515P .

PR 07-JUN-2000; 2000US-0203467P .

PR 28-JUN-2000; 2000US-021148P .

PR 07-JUL-2000; 2000US-0215135P .

PR 07-JUL-2000; 2000US-0216547P .

PR 07-JUL-2000; 2000US-0216880P .

PR 11-JUL-2000; 2000US-0217487P .

PR 14-JUL-2000; 2000US-0217496P .

PR 26-JUL-2000; 2000US-0220963P .

PR 26-JUL-2000; 2000US-0220964P .

PR 14-AUG-2000; 2000US-0224564P .

PR 14-AUG-2000; 2000US-0224518P .

PR 14-AUG-2000; 2000US-0224519P .

PR 14-AUG-2000; 2000US-0225113P .

PR 14-AUG-2000; 2000US-0225114P .

PR 14-AUG-2000; 2000US-0225166P .

PR 14-AUG-2000; 2000US-0225167P .

PR 14-AUG-2000; 2000US-0225270P .

PR 14-AUG-2000; 2000US-0225447P .

PR 14-AUG-2000; 2000US-0225457P .

PR 14-AUG-2000; 2000US-0225758P .

PR 14-AUG-2000; 2000US-0225759P .  
PR 18-AUG-2000; 2000US-0226279P .  
PR 22-AUG-2000; 2000US-0226681P .  
PR 22-AUG-2000; 2000US-0226868P .  
PR 23-AUG-2000; 2000US-022182P .  
PR 30-AUG-2000; 2000US-0221009P .  
PR 01-SEP-2000; 2000US-0229287P .  
PR 01-SEP-2000; 2000US-0223434P .  
PR 01-SEP-2000; 2000US-0229344P .  
PR 05-SEP-2000; 2000US-0229509P .  
PR 05-SEP-2000; 2000US-0229513P .  
PR 06-SEP-2000; 2000US-02310437P .  
PR 06-SEP-2000; 2000US-0230438P .  
PR 08-SEP-2000; 2000US-0231242P .  
PR 08-SEP-2000; 2000US-0231243P .  
PR 08-SEP-2000; 2000US-0231413P .  
PR 08-SEP-2000; 2000US-0232080P .  
PR 08-SEP-2000; 2000US-0231081P .  
PR 12-SEP-2000; 2000US-0231240P .  
PR 14-SEP-2000; 2000US-0232397P .  
PR 14-SEP-2000; 2000US-0232398P .  
PR 14-SEP-2000; 2000US-0231399P .  
PR 14-SEP-2000; 2000US-0231414P .  
PR 14-SEP-2000; 2000US-0232080P .  
PR 14-SEP-2000; 2000US-0231968P .  
PR 14-SEP-2000; 2000US-0231244P .  
PR 14-SEP-2000; 2000US-0231413P .  
PR 14-SEP-2000; 2000US-0232397P .  
PR 14-SEP-2000; 2000US-0232398P .  
PR 14-SEP-2000; 2000US-0231399P .  
PR 14-SEP-2000; 2000US-0231401P .  
PR 14-SEP-2000; 2000US-0231063P .  
PR 14-SEP-2000; 2000US-0233064P .  
PR 14-SEP-2000; 2000US-0233065P .  
PR 21-SEP-2000; 2000US-0234223P .  
PR 21-SEP-2000; 2000US-0234274P .  
PR 25-SEP-2000; 2000US-0234997P .  
PR 26-SEP-2000; 2000US-0235484P .  
PR 27-SEP-2000; 2000US-0235834P .  
PR 27-SEP-2000; 2000US-0235836P .  
PR 29-SEP-2000; 2000US-0236327P .  
PR 29-SEP-2000; 2000US-0236367P .  
PR 29-SEP-2000; 2000US-0236368P .  
PR 29-SEP-2000; 2000US-0236369P .  
PR 02-OCT-2000; 2000US-023370P .  
PR 02-OCT-2000; 2000US-023710P .  
PR 02-OCT-2000; 2000US-0236802P .  
PR 02-OCT-2000; 2000US-0237037P .  
PR 02-OCT-2000; 2000US-0231039P .  
PR 02-OCT-2000; 2000US-0237140P .  
PR 13-OCT-2000; 2000US-023935P .  
PR 13-OCT-2000; 2000US-023937P .  
PR 20-OCT-2000; 2000US-0241809P .  
PR 20-OCT-2000; 2000US-0241826P .  
PR 20-OCT-2000; 2000US-0242221P .  
PR 01-NOV-2000; 2000US-0244617P .  
PR 08-NOV-2000; 2000US-0246523P .  
PR 08-NOV-2000; 2000US-0246524P .  
PR 08-NOV-2000; 2000US-024525P .  
PR 08-NOV-2000; 2000US-0246476P .  
PR 08-NOV-2000; 2000US-0246477P .  
PR 08-NOV-2000; 2000US-024478P .  
PR 08-NOV-2000; 2000US-0244617P .  
PR 08-NOV-2000; 2000US-0246532P .  
PR 08-NOV-2000; 2000US-0246609P .  
PR 08-NOV-2000; 2000US-0246610P .



PR 08-SEP-2000; 2000US-02311242P.  
 PR 08-SEP-2000; 2000US-02311243P.  
 PR 08-SEP-2000; 2000US-02311244P.  
 PR 08-SEP-2000; 2000US-0231113P.  
 PR 08-SEP-2000; 2000US-0231114P.  
 PR 08-SEP-2000; 2000US-0231141P.  
 PR 08-SEP-2000; 2000US-023208P.  
 PR 12-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0233399P.  
 PR 14-SEP-2000; 2000US-023400P.  
 PR 14-SEP-2000; 2000US-0234201P.  
 PR 14-SEP-2000; 2000US-0231063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-02333065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234327P.  
 PR 25-SEP-2000; 2000US-02343997P.  
 PR 26-SEP-2000; 2000US-0234998P.  
 PR 27-SEP-2000; 2000US-0235134P.  
 PR 29-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 02-OCT-2000; 2000US-023639P.  
 PR 02-OCT-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-023707P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 13-OCT-2000; 2000US-0231935P.  
 PR 13-OCT-2000; 2000US-0239337P.  
 PR 20-OCT-2000; 2000US-024096P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 01-NOV-2000; 2000US-0241786P.  
 PR 08-NOV-2000; 2000US-0241787P.  
 PR 08-NOV-2000; 2000US-0241108P.  
 PR 08-NOV-2000; 2000US-0241809P.  
 PR 08-NOV-2000; 2000US-024198P.  
 PR 01-NOV-2000; 2000US-024221P.  
 PR 08-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0244647P.  
 PR 08-NOV-2000; 2000US-0244678P.  
 PR 08-NOV-2000; 2000US-024523P.  
 PR 08-NOV-2000; 2000US-024524P.  
 PR 08-NOV-2000; 2000US-024625P.  
 PR 08-NOV-2000; 2000US-024526P.  
 PR 08-NOV-2000; 2000US-024527P.  
 PR 08-NOV-2000; 2000US-024528P.  
 PR 08-NOV-2000; 2000US-024532P.  
 PR 08-NOV-2000; 2000US-024609P.  
 PR 17-NOV-2000; 2000US-0246610P.  
 PR 17-NOV-2000; 2000US-0246611P.  
 PR 17-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 01-DEC-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-02510391P.  
 PR 01-DEC-2000; 2000US-0251160P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen Ca, Barash SC, Ruben SM;  
 XX WPI: 2001-541565/60.  
 XX DR  
 XX PT Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.  
 XX PT Disclosure; SEQ ID NO 6803; 1701PP + Sequence Listing; English.  
 XX PS  
 XX CC The invention relates to novel genes (ABA1104-ABA21534) and proteins (ABA14678-ABA18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX SQ Sequence 1191 BP; 335 A; 265 C; 279 G; 312 T; 0 U; 0 Other;  
 Query Match 68.2%; Score 15; DB 5; Length 1191;  
 Best Local Similarity 80.0%; Pred. No. 29;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 CACUCGUGGGCGCTT 22  
 Db 756 CACTGTGAGCTCTT 770  
 RESULT 15  
 AA122168/C  
 ID AA122168 standard; DNA; 1820 BP.  
 XX AC  
 XX DT 12-OCT-2001 (first entry)  
 DB Probe #12101 for gene expression analysis in human cervical cell sample.  
 KW Probe; human; microarray; gene expression; cervical epithelial cell;  
 KW cervical cancer; ss.

XX Homo sapiens.  
OS Homo sapiens.  
PN WO200157278-A2.  
XX PD 09-AUG-2001.  
XX PF 30-JAN-2001; 2001WO-US000670.  
XX PR 04-FEB-2000; 2000US-0180312P.  
XX PR 26-MAY-2000; 2000US-020745P.  
XX PR 30-JUN-2000; 2000US-020745P.  
XX PR 03-AUG-2000; 2000US-00632365.  
XX PR 21-SEP-2000; 2000US-0234687P.  
XX PR 27-SEP-2000; 2000US-0234687P.  
XX PR 04-OCT-2000; 2000US-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.  
PA XX  
PA PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX DR WPI; 2001-483447/52.  
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.  
XX PT  
XX PS Claim 4; SEQ ID NO 15552; 639pp + Sequence Listing; English.  
XX PA  
XX The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human foetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

(MOLE-) MOLECULAR DYNAMICS INC.  
PA XX  
PA PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX DR WPI; 2001-488901/53.  
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.  
XX PS Claim 25; SEQ ID NO 12101; 487pp; English.  
XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;  
XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;  
XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

(MOLE-) MOLECULAR DYNAMICS INC.  
PA XX  
PA PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX DR WPI; 2001-488901/53.  
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.  
XX PS Claim 25; SEQ ID NO 12101; 487pp; English.  
XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;  
XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

(MOLE-) MOLECULAR DYNAMICS INC.  
PA XX  
PA PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX DR WPI; 2001-488901/53.  
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human Placenta.

XX Claim 25; SEQ ID NO 16153; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SNP).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders.

XX Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;  
 Best Local Similarity 80.0%; Pred. No. 30;  
 Matches 12; Conservative 3; Nismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGAGGUCU<sup>T</sup> 22

Db 1774 CACTGTGAGCTT 1760

RESULT 18  
 ABA49335\_C  
 ID ABA49335 standard; DNA; 1820 BP.

XX  
 AC ABA49335;  
 XX DT 01-FEB-2002 (first entry)  
 DE Human breast cell single exon nucleic acid probe #8030.  
 XX Human; microarray; single exon probe; gene expression; breast; disease;  
 KW cancer; ss.  
 XX OS Homo sapiens.  
 XX PN WO2015771-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US000662.

XX PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-0207456P.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-00632366.  
 PR 27-SEP-2000; 2000US-0234687P.  
 PR 04-OCT-2000; 2000US-0234687P.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-496933/54.  
 XX PT New spatially-addressable set of single exon nucleic acid probes, useful  
 PT for measuring gene expression in sample derived from human breast,  
 PT comprises number of single exon nucleic acid probes.

XX PS Claim 4; SEQ ID NO 8030; 327bp + Sequence Listing; English.  
 XX PT The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human breast and BT 474 cells. The method involves contacting the  
 CC probes with a collection of detectably labelled nucleic acids derived  
 CC from mRNA of human breast, and then measuring the label bound to each  
 CC probe of the microarray. The probes are useful for verifying the  
 CC expression of regions of genomic DNA predicted to encode proteins. They  
 CC are useful for gene discovery, and for determining predisposition and/or  
 CC prognosis breast disease. Gene expression analysis is useful for  
 CC assessing the toxicity of chemical agents on cells. The microarray of  
 CC this invention presents a far greater diversity of probes for measuring  
 CC gene expression, with far less bias than expressed sequence tag

CC microarrays. The method is suitable for rapid production of functional  
 CC information from genomic sequence. The present sequence is a single exon  
 CC nucleic acid probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp://wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;  
 Best Local Similarity 80.0%; Pred. No. 30;  
 Matches 12; Conservative 3; Nismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGAGGUCU<sup>T</sup> 22

Db 1774 CACTGTGAGCTT 1760

RESULT 19  
 ABA34342\_C  
 ID ABA34342 standard; DNA; 1820 BP.

XX AC ABA34342;  
 XX DT 23-JAN-2002 (first entry)

XX DB Probe #12808 for gene expression analysis in human heart cell sample.  
 XX Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 congenital heart disease; ss.  
 XX OS Homo sapiens.

XX PN WO200157274-A2.  
 XX PD 09-AUG-2001.  
 XX PP 30-JAN-2001; 2001WO-US000666.

XX PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00632366.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0234687P.  
 PR 04-OCT-2000; 2000US-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-488899/53.

XX PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts.

XX PS Claim 4; SEQ ID NO 12808; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart. The  
 CC present sequence is one such probe. The probes may be used for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from the human heart via microarrays. By measuring gene expression, the  
 CC probes are useful for predicting, diagnosing, grading, staging,  
 CC monitoring and prognosing diseases of the human heart and vascular system  
 e.g. cardiovascular disease. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp://wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match Score 15; DB 4; Length 1820;  
 Best Local Similarity 80.0%; Pred. No. 30;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 AC XX  
 DT 09-OCT-2001 (first entry)

Probe #7860 used to measure gene expression in human breast sample.

KW Probe; human; breast disease; breast cancer; development disorder; ss;  
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.  
 KW XX  
 OS Homo sapiens.  
 XX  
 PN WO200157270-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PP 29-JAN-2001; 2001WO-US000661.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 03-JUN-2000; 2000US-00632366.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR 2001-476286/51.

Novel single exon nucleic acid probe used to measuring gene expression in a human breast.

PT Claim 25; SEQ ID NO 7860; 322pp; English.

XX  
 XX  
 CC The present invention relates to novel single exon nucleic acid probes.  
 CC The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosis diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include; breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/patent/applications/search/pct](http://wipo.int/patent/applications/search/pct)

CC SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;  
 CC Query Match Score 15; DB 5; Length 1820;  
 CC Best Local Similarity 80.0%; Pred. No. 30;  
 CC Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 CC AC XX  
 CC DT 19-AUG-2002 (first entry)

Human genome-derived single exon probe ORF from lung SEQ ID No 15429.

RESULT 22  
 ABS15429/C  
 ID ABS15429 standard; DNA; 1820 BP.  
 AC XX  
 AC ABS15429;  
 XX  
 DB XX  
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

RESULT 21  
 AA107869/C  
 ID AA107869 standard; DNA; 1820 BP.  
 XX



RESULT 24  
 ABA69247/C  
 ID ABA69247 standard; DNA; 1870 BP.  
 XX  
 AC ABA69247;  
 XX DT 01-FEB-2002 (first entry)  
 XX Human foetal liver single exon nucleic acid probe #17552.  
 DE XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 KW XX Homo sapiens.  
 OS XX WO20015277-A2.  
 PN XX PD 09-AUG-2001.  
 XX PP 30-JAN-2001; 2001WO-US0006669.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236355P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-488897/53.  
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 gene expression in human placenta.  
 XX P5 Claim 25; SEQ ID NO 18106; 654pp; English.  
 XX CC The present invention relates to single exon nucleic acid probes (SENP).  
 CC The present sequence is one such probe. The probes are useful for  
 producing a microarray for predicting, measuring and displaying gene  
 expression in samples derived from human placenta. The probes are useful  
 for antenatal diagnosis of human genetic disorders  
 XX SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;  
 XX Query Match 68.2%; Score 15; DB 4; Length 1870;  
 PT Best Local Similarity 80.0%; Pred. No. 30;  
 PT Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 XX PS QV 8 CACUCGUGAGCUCUTT 22  
 XX CC The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
 XX SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;  
 XX Query Match 68.2%; Score 15; DB 4; Length 1870;  
 PT Best Local Similarity 80.0%; Pred. No. 30;  
 PT Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 XX PS QV 8 CACUCGUGAGCUCUTT 22  
 XX Db 1774 CACTCGTAGCTCTT 1760  
 XX Homo sapiens.  
 XX OS WO20015271-A2.  
 XX PN  
 XX PD 09-AUG-2001.  
 XX PP 30-JAN-2001; 2001WO-US0006662.  
 XX AC AA149420;  
 XX DT 17-OCT-2001 (first entry)  
 XX DE Probe #18106 used to measure gene expression in human placenta sample.  
 KW XX Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.  
 OS XX Homo sapiens.

RESULT 25  
 AA149420/C  
 ID AA149420 standard; DNA; 1870 BP.  
 XX  
 AC AA149420;  
 XX DT 17-OCT-2001 (first entry)  
 XX DE Probe #18106 used to measure gene expression in human placenta sample.  
 KW XX Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.  
 OS XX Homo sapiens.

XX	Penn SG,	Hanzel DK,	Chen W,	Rank DR;	PI	Penn SG,	Hanzel DK,	Chen W,	Rank DR;	
PI	XX	WPT,	2001-48899/53.	DR	XX	WPT,	2001-48899/53.	DR	XX	
DR	XX	New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, useful comprises number of single exon nucleic acid probes.	PT	PT	PT	Single exon nucleic acid probes for analyzing gene expression in human hearts.	PT	PT	XX	
XX	PS	Claim 4; SEQ ID NO 14629; 530pp; English.	XX	XX	XX	Claim 4; SEQ ID NO 14629; 530pp; English.	XX	XX	XX	
XX	CC	The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognostic diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	CC	CC	CC	The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognostic diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	CC	CC	CC	CC
XX	SQ	Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;	SQ	Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;	SQ	Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;	SQ	Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;	XX	
XX	Query Match	68.2%; Score 15; DB 4;	Query Match	68.2%; Score 15; DB 4;	Query Match	68.2%; Score 15; DB 4;	Query Match	68.2%; Score 15; DB 4;	XX	
XX	Best Local Similarity	80.0%; Pred. No. 30;	Best Local Similarity	80.0%; Pred. No. 30;	Best Local Similarity	80.0%; Pred. No. 30;	Best Local Similarity	80.0%; Pred. No. 30;	XX	
XX	Matches	12; Conservative	Matches	12; Conservative	Matches	12; Conservative	Matches	12; Conservative	XX	
XX	Qy	8 CACUGUGAGCUCTT 22	Qy	8 CACUGUGAGCUCTT 22	Qy	8 CACUGUGAGCUCTT 22	Qy	8 CACUGUGAGCUCTT 22	XX	
XX	Db	1774 CACTCGTGAGCTCTT 1760	Db	1774 CACTCGTGAGCTCTT 1760	Db	1774 CACTCGTGAGCTCTT 1760	Db	1774 CACTCGTGAGCTCTT 1760	XX	
XX	RESULT 28		XX	RESULT 28	XX	RESULT 28	XX	RESULT 28	XX	
XX	ID	AAK43349_C	ID	AAK43349 standard	ID	AAK43349 standard	ID	AAK43349 standard	ID	
XX	AC		XX	AC	XX	AC	XX	AC	XX	
XX	DE		XX	DE	XX	DE	XX	DE	XX	
XX	XX		XX	XX	XX	XX	XX	XX	XX	
XX	KW		XX	KW	XX	KW	XX	KW	XX	
XX	microarray; cancer; leukaemia; lymphoma; myeloma; ss.		XX	microarray; cancer; leukaemia; lymphoma; myeloma; ss.	XX	microarray; cancer; leukaemia; lymphoma; myeloma; ss.	XX	microarray; cancer; leukaemia; lymphoma; myeloma; ss.	XX	
XX	Homo sapiens.		XX	Homo sapiens.	XX	Homo sapiens.	XX	Homo sapiens.	XX	
XX	OS		XX	OS	XX	OS	XX	OS	XX	
XX	XX		XX	XX	XX	XX	XX	XX	XX	
XX	PR		XX	PR	XX	PR	XX	PR	XX	
XX	04-FEB-2000; 2000US-0180312P.		XX	04-FEB-2000; 2000US-0180312P.		XX	XX	XX	XX	
XX	26-MAY-2000; 2000US-0207456P.		XX	26-MAY-2000; 2000US-0207456P.		XX	XX	XX	XX	
XX	PR		XX	PR	XX	PR	XX	PR	XX	
XX	30-JUN-2000; 2000US-00608408.		XX	30-JUN-2000; 2000US-00608408.		XX	XX	XX	XX	
XX	PR		XX	PR	XX	PR	XX	PR	XX	
XX	03-AUG-2000; 2000US-00532366.		XX	03-AUG-2000; 2000US-00532366.		XX	XX	XX	XX	
XX	PR		XX	PR	XX	PR	XX	PR	XX	
XX	21-SEP-2000; 2000US-0234687P.		XX	21-SEP-2000; 2000US-0234687P.		XX	XX	XX	XX	
XX	PR		XX	PR	XX	PR	XX	PR	XX	
XX	27-SEP-2000; 2000US-0236359P.		XX	27-SEP-2000; 2000US-0236359P.		XX	XX	XX	XX	
XX	PR		XX	PR	XX	PR	XX	PR	XX	
XX	04-OCT-2000; 2000GB-00024263.		XX	04-OCT-2000; 2000GB-00024263.		XX	XX	XX	XX	
XX	(MOLE-) MOLECULAR DYNAMICS INC.		XX	(MOLE-) MOLECULAR DYNAMICS INC.		XX	XX	(MOLE-) MOLECULAR DYNAMICS INC.	XX	
XX	PA		XX	PA		XX	XX	PA	XX	
XX	PI		XX	PI		XX	XX	PI	XX	
XX	Penn SG,	Hanzel DK,	Chen W,	Rank DR;	PI	Penn SG,	Hanzel DK,	Chen W,	Rank DR;	
XX	WPT,	2001-48899/53.	DR	DR	XX	WPT,	2001-48899/53.	DR	XX	
XX	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.		XX	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.		XX	XX	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.	XX	
XX	Example 4; SEQ ID NO 17906; 658pp + Sequence Listing; English.		XX	Example 4; SEQ ID NO 17906; 658pp + Sequence Listing; English.		XX	XX	Example 4; SEQ ID NO 17906; 658pp + Sequence Listing; English.	XX	
XX	The present invention provides a number of single exon nucleic acid		XX	The present invention provides a number of single exon nucleic acid		XX	XX	The present invention provides a number of single exon nucleic acid	XX	



CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 1201 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis,  
CC Kartagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a single exon probe open reading frame of the  
CC invention. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

XX  
SQ Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;  
Query Match 68.2%; Score 15; DB 6; Length 1870;  
Best Local Similarity 80.0%; Pred. No. 30;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Oy 8 CACUUGUGAGCUU 22  
Db 1774 CACTGGTGAAGTCCT 1760

Search completed: July 20, 2005, 23:34:20  
Job time : 455 secs

THIS PAGE IS BLANK

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:37:01 ; Search time 3090 Seconds

(without alignments)  
 271.008 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaaucacucugagggcucc 22

Scoring table: OLIGO\_NUC

Gappop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 300 summaries

Database : EST:\*

```
1: 9b_est1:*
2: 9b_est2:*
3: 9b_hnc:*
4: 9b_est3:*
5: 9b_est4:*
6: 9b_est5:*
7: 9b_est6:*
8: 9b_gss1:*
9: 9b_gss2:*
```

Post-processing: Listing first 300 summaries

Database : EST:\*

```
1: 9b_est1:*
2: 9b_est2:*
3: 9b_hnc:*
4: 9b_est3:*
5: 9b_est4:*
6: 9b_est5:*
7: 9b_est6:*
8: 9b_gss1:*
9: 9b_gss2:*
```

Pre! No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

% Query Score Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
C 1	17	77.3	1344	4	BG917388	602816903	CG929001 30DGS--06
C 2	16	72.7	200	7	CF296001	CF29826 7LEAF--04	CF29826 7LEAF--04
C 3	16	72.7	206	7	CF298930	CF298930 7LEAF--02	CF298930 7LEAF--02
C 4	16	72.7	245	7	BE228712	BE228712 98AS1025	BE228712 98AS1025
C 5	16	72.7	270	2	CF295034	CF295034 30DGS--04	CF295034 30DGS--04
C 6	16	72.7	272	7	CF299062	CF299062 7LEAF--02	CF299062 7LEAF--02
C 7	16	72.7	273	7	CF300491	CF300491 7LEAF--04	CF300491 7LEAF--04
C 8	16	72.7	273	7	CF302576	CF302576 7LEAF--08	CF302576 7LEAF--08
C 9	16	72.7	276	7	CF30259	CF30259 7LEAF--04	CF30259 7LEAF--04
C 10	16	72.7	277	7	CF298981	CF298981 7LEAF--02	CF298981 7LEAF--02
C 11	16	72.7	281	7	CF298536	CF298536 7LEAF--01	CF298536 7LEAF--01
C 12	16	72.7	283	7	CF294911	CF294911 30DGS--04	CF294911 30DGS--04
C 13	16	72.7	311	7	CF299932	CF299932 7LEAF--04	CF299932 7LEAF--04
C 14	16	72.7	313	6	CB668085	CB668085 OSTNED15M	CB668085 OSTNED15M
C 15	16	72.7	315	7	CF30735	CF30735 7LEAF--05	CF30735 7LEAF--05
C 16	16	72.7	321	7	CF300267	CF300267 7LEAF--04	CF300267 7LEAF--04
C 17	16	72.7	321	7	CF334972	CF334972 JMT--04-H	CF334972 JMT--04-H
C 18	16	72.7	324	7	CF301775	CF301775 7LEAF--06	CF301775 7LEAF--06
C 19	16	72.7	326	7	CF295052	CF295052 30DGS--04	CF295052 30DGS--04
C 20	16	72.7	326	7	CF300479	CF300479 7LEAF--04	CF300479 7LEAF--04
C 21	16	72.7	329	7	CF302299	CF302299 7LEAF--06	CF302299 7LEAF--06
C 22	16	72.7	330	7	CF301705	CF301705 7LEAF--06	CF301705 7LEAF--06
C 23	16	72.7	340	7	CF299101	CF299101 7LEAF--02	CF299101 7LEAF--02
C 24	16	72.7	342	7	CF294601	CF294601 30DGS--04	CF294601 30DGS--04

C 25	16	72.7	343	7	CF300860	CF300860 7LEAF--05	CF300860 7LEAF--05
C 26	16	72.7	349	4	CP302208	CP302208 BI1810487	CP302208 BI1810487
C 27	16	72.7	350	4	BI1810487	BI1810487 JMT--03-O	BI1810487 JMT--03-O
C 28	16	72.7	350	7	CF333339	CF333339 JMT--03-A	CF333339 JMT--03-A
C 29	16	72.7	351	7	CF300557	CF300557 CF301059	CF300557 CF301059
C 30	16	72.7	352	7	CF301059	CF301059 7LEAF--05	CF301059 7LEAF--05
C 31	16	72.7	353	7	CF294342	CF294342 CF293314	CF294342 CF293314
C 32	16	72.7	358	7	CF293314	CF293314 30DGS--04	CF293314 30DGS--04
C 33	16	72.7	358	7	CF30146	CF30146 CF30125	CF30146 CF30125
C 34	16	72.7	359	7	CF30125	CF30125 CF295099	CF30125 CF295099
C 35	16	72.7	360	7	CF295099	CF295099 30DGS--04	CF295099 30DGS--04
C 36	16	72.7	361	7	CF293177	CF293177 CF333477	CF293177 CF333477
C 37	16	72.7	361	7	CF333477	CF333477 CF294625	CF333477 CF294625
C 38	16	72.7	363	7	CF294625	CF294625 CF293314	CF294625 CF293314
C 39	16	72.7	364	4	BI797027	BI797027 H062C08 E	BI797027 H062C08 E
C 40	16	72.7	364	7	CF294149	CF294149 CF294128	CF294149 CF294128
C 41	16	72.7	364	7	CF300473	CF300473 CF294128	CF300473 CF294128
C 42	16	72.7	365	7	CF302440	CF302440 CF294128	CF302440 CF294128
C 43	16	72.7	366	7	CF298089	CF298089 CF294128	CF298089 CF294128
C 44	16	72.7	367	7	CF3344002	CF3344002 JMT--03-C	CF3344002 JMT--03-C
C 45	16	72.7	368	7	CF293465	CF293465 CF294128	CF293465 CF294128
C 46	16	72.7	368	7	CF294128	CF294128 CF294128	CF294128 CF294128
C 47	16	72.7	369	7	CF294128	CF294128 CF294128	CF294128 CF294128
C 48	16	72.7	372	7	CF334668	CF334668 CF294128	CF334668 CF294128
C 49	16	72.7	373	7	CF298819	CF298819 CF294128	CF298819 CF294128
C 50	16	72.7	373	7	CF299944	CF299944 CF294128	CF299944 CF294128
C 51	16	72.7	381	7	CF301512	CF301512 CF294128	CF301512 CF294128
C 52	16	72.7	381	7	CF294128	CF294128 CF294128	CF294128 CF294128
C 53	16	72.7	388	7	CF333248	CF333248 JMT--02-B	CF333248 JMT--02-B
C 54	16	72.7	389	2	BE228607	BE228607 CF294128	BE228607 CF294128
C 55	16	72.7	389	7	CF296172	CF296172 CF294128	CF296172 CF294128
C 56	16	72.7	389	7	CF302115	CF302115 CF294128	CF302115 CF294128
C 57	16	72.7	391	7	CF279865	CF279865 14ETL--06	CF279865 14ETL--06
C 58	16	72.7	394	7	CF292228	CF292228 30DGS--01	CF292228 30DGS--01
C 59	16	72.7	396	7	CF2931499	CF2931499 30DGS--01	CF2931499 30DGS--01
C 60	16	72.7	397	7	CF295574	CF295574 CF294128	CF295574 CF294128
C 61	16	72.7	398	7	CF281031	CF281031 14ETL--06	CF281031 14ETL--06
C 62	16	72.7	400	7	CF293653	CF293653 30DGS--02	CF293653 30DGS--02
C 63	16	72.7	400	7	CF301091	CF301091 7LEAF--05	CF301091 7LEAF--05
C 64	16	72.7	402	7	CF292298	CF292298 30DGS--01	CF292298 30DGS--01
C 65	16	72.7	402	7	CF301882	CF301882 CF294128	CF301882 CF294128
C 66	16	72.7	402	7	CF333799	CF333799 CF294128	CF333799 CF294128
C 67	16	72.7	404	7	CF293371	CF293371 CF294128	CF293371 CF294128
C 68	16	72.7	405	7	CF292038	CF292038 14ROOT--00	CF292038 14ROOT--00
C 69	16	72.7	406	7	CF291160	CF291160 CF294128	CF291160 CF294128
C 70	16	72.7	407	7	CF295556	CF295556 30DGS--06	CF295556 30DGS--06
C 71	16	72.7	409	7	CF297322	CF297322 30DGS--08	CF297322 30DGS--08
C 72	16	72.7	412	7	CF30167	CF30167 CF294128	CF30167 CF294128
C 73	16	72.7	412	7	CF292334	CF292334 30DGS--01	CF292334 30DGS--01
C 74	16	72.7	414	7	CF292393	CF292393 30DGS--01	CF292393 30DGS--01
C 75	16	72.7	415	7	CF317419	CF317419 HD--07-B1	CF317419 HD--07-B1
C 76	16	72.7	417	7	CF298484	CF298484 7LEAF--08	CF298484 7LEAF--08
C 77	16	72.7	417	7	CF3337043	CF3337043 JMT--07-F	CF3337043 JMT--07-F
C 78	16	72.7	419	7	CF310192	CF310192 ABF--04-L	CF310192 ABF--04-L
C 79	16	72.7	420	6	CA752317	CA752317 CA752323	CA752317 CA752323
C 80	16	72.7	420	6	CA752323	CA752323 JSYLA71 R	CA752323 JSYLA71 R
C 81	16	72.7	421	6	CA753899	CA753899 JSYLA74 R	CA753899 JSYLA74 R
C 82	16	72.7	421	7	CF293078	CF293078 30DGS--06	CF293078 30DGS--06
C 83	16	72.7	423	7	CF301435	CF301435 30DGS--06	CF301435 30DGS--06
C 84	16	72.7	424	2	AW069361	AW069361 migie1002A	AW069361 migie1002A
C 85	16	72.7	424	2	CF293077	CF293077 30DGS--04	CF293077 30DGS--04
C 86	16	72.7	427	7	CF335603	CF335603 JMT--05-F	CF335603 JMT--05-F
C 87	16	72.7	427	7	CF300099	CF300099 30DGS--03	CF300099 30DGS--03
C 88	16	72.7	428	7	CF302576	CF302576 7LEAF--08	CF302576 7LEAF--08
C 89	16	72.7	428	7	CF301435	CF301435 30DGS--06	CF301435 30DGS--06
C 90	16	72.7	431	7	CF293115	CF293115 30DGS--02	CF293115 30DGS--02
C 91	16	72.7	431	7	CF295077	CF295077 30DGS--04	CF295077 30DGS--04
C 92	16	72.7	431	7	CF335603	CF335603 JMT--05-F	CF335603 JMT--05-F
C 93	16	72.7	433	7	CF299231	CF299231 30DGS--03	CF299231 30DGS--03
C 94	16	72.7	434	4	BM038487	BM038487 7LEAF--03	BM038487 7LEAF--03
C 95	16	72.7	434	4	BI795494	BI795494 H023107 E	BI795494 H023107 E
C 96	16	72.7	435	7	CP297684	CP297684 30DGS--08	CP297684 30DGS--08
C 97	16	72.7	436	7	CF333485	CF333485 JMT--02-G	CF333485 JMT--02-G

C 98	16	72.7	437	7	CF300287	7LEAF--04	CP335971	JMT--05-N
C 99	16	72.7	438	7	CF300287	7LEAF--06-O	CP335871	JMT--05-L
C 100	16	72.7	439	7	CF336454	JMT--06-T	CP202098	7LEAF--07
C 101	16	72.7	440	4	BI181469	J009B04 O	CP336032	JMT--05-P
C 102	16	72.7	443	7	CF298634	7LEAF--02	CP294456	30DGS--03
C 103	16	72.7	443	7	CF326605	JMT1--06-	CP201786	7LEAF--06
C 104	16	72.7	444	7	CP296710	10DGS--07	CP336909	JMT--07-C
C 105	16	72.7	447	7	CP300126	7LEAF--04	CP222748	30DGS--04
C 106	16	72.7	447	7	CF334006	JMT--03-C	CP299949	7LEAF--04
C 107	16	72.7	447	7	CP35012	JMT--04-I	CP36522	JMT--06-J
C 108	16	72.7	448	7	CF296222	30DGS--01	CP300189	7LEAF--03
C 109	16	72.7	448	7	CF298719	7LEAF--02	CP302481	7LEAF--04
C 110	16	72.7	452	7	CF299336	7LEAF--03	CP335479	JMT--05-C
C 111	16	72.7	454	7	CP307856	ABF--01-H	CP294477	30DGS--04
C 112	16	72.7	455	7	CF298335	7LEAF--01	CP297419	30DGS--08
C 113	16	72.7	455	7	CP333435	JMT--02-F	BO907486	P007C11 O
C 114	16	72.7	459	7	CP295831	30DGS--05	CP2996926	30DGS--07
C 115	16	72.7	459	7	CP292622	30DGS--01	CP299465	7LEAF--03
C 116	16	72.7	460	4	BI180599	A006C09 O	CP301879	7LEAF--04
C 117	16	72.7	460	4	BI180599	A006C12 O	CP332788	JMT--01-G
C 118	16	72.7	461	7	CF291539	ABF--1.1	CP332942	JMT--01-K
C 119	16	72.7	462	7	CF295701	JMT--06-M	CP335956	JMT--01-N
C 120	16	72.7	462	7	CP297362	30DGS--05	CP336502	JMT--06-J
C 121	16	72.7	462	7	CP302341	7LEAF--03	CP299465	7LEAF--03
C 122	16	72.7	463	7	CP295676	30DGS--05	CP300694	7LEAF--03-C
C 123	16	72.7	464	7	CP290575	30DGS--04	CP334025	JMT--03-C
C 124	16	72.7	464	7	CF298102	7LEAF--01	CP34152	JMT--03-F
C 125	16	72.7	466	7	CF333098	JMT--01-N	CP335291	JMT--04-O
C 126	16	72.7	466	7	CP36355	JMT--06-G	CP335896	JMT--05-M
C 127	16	72.7	467	7	CF299260	30DGS--03	BQ529578	h12-t3 .se
C 128	16	72.7	467	7	CP295676	30DGS--05	CP333698	JMT--02-L
C 129	16	72.7	467	7	CF298470	7LEAF--03	CP34025	JMT--03-A
C 130	16	72.7	467	7	CP332819	JMT--01-H	CP34152	JMT--03-G
C 131	16	72.7	467	7	CF298102	JMT--08-L	CP335291	JMT--04-G
C 132	16	72.7	469	7	CF333098	JMT--01-N	CP335896	JMT--05-M
C 133	16	72.7	470	7	CF298227	7LEAF--04	CP312560	ABF--08-F
C 134	16	72.7	470	7	CP302203	7LEAF--01	CP337598	JMT--08-F
C 135	16	72.7	472	7	CF297460	30DGS--08	CP208990	ABF--03-A
C 136	16	72.7	472	7	CF333330	JMT--02-D	CP336371	JMT--06-G
C 137	16	72.7	473	7	CF334916	JMT--04-G	CP302018	7LEAF--05
C 138	16	72.7	474	7	CF334574	JMT--06-N	CP302471	7LEAF--08
C 139	16	72.7	474	7	CF334359	JMT--03-K	CP312560	ABF--08-F
C 140	16	72.7	474	7	CF334359	JMT--05-F	CP333698	JMT--08-C
C 141	16	72.7	474	7	BI180799	G002A04 O	AA753360	977AS2393
C 142	16	72.7	475	7	CF333611	JMT--02-J	BQ97567	P008G11 O
C 143	16	72.7	475	7	CF300208	7LEAF--04	CP301004	7LEAF--05
C 144	16	72.7	475	7	CF298227	7LEAF--01	CP335313	JMT--04-P
C 145	16	72.7	475	7	CP302203	7LEAF--07	CP312560	JMT--07-J
C 146	16	72.7	477	7	CF297460	30DGS--08	CP296585	30DGS--07
C 147	16	72.7	477	7	CF333615	JMT--05-P	CP333254	JMT--02-B
C 148	16	72.7	478	7	CF333127	JMT--01-H	CP336913	JMT--07-C
C 149	16	72.7	478	7	CF333330	JMT--02-D	CP295579	30DGS--05
C 150	16	72.7	478	7	CF330403	JMT--08-L	CP302633	7LEAF--08
C 151	16	72.7	479	2	BI430561	GO2AC02T3	CP334079	JMT--03-D
C 152	16	72.7	479	2	CF102933	R008F02 O	CP335590	JMT--02-E
C 153	16	72.7	480	4	BM419049	CP297412	CP334927	JMT--04-G
C 154	16	72.7	480	7	BI180799	G002A04 O	CP312061	ABF--07-J
C 155	16	72.7	481	7	CF332849	ABF--08-M	CP333207	JMT--02-A
C 156	16	72.7	481	7	CF330803	JMT--04-J	CP336446	JMT--06-I
C 157	16	72.7	484	7	CF297887	7LEAF--01	CP29988	99AS225 R
C 158	16	72.7	484	7	CP202376	7LEAF--08	CP300116	7LEAF--04
C 159	16	72.7	484	7	CF334479	JMT--03-M	CP336057	7LEAF--05
C 160	16	72.7	484	7	CF335350	JMT--04-P	CP337639	JMT--08-C
C 161	16	72.7	485	7	CF102641	7LEAF--08	CP294297	30DGS--03
C 162	16	72.7	485	7	CF336484	JMT--06-I	CP295780	30DGS--04
C 163	16	72.7	486	7	CF298252	30DGS--05	CP33862	JMT--08-H
C 164	16	72.7	486	7	CF297412	JMT--03-C	CP337639	JMT--08-C
C 165	16	72.7	486	7	CF295637	JMT--04-N	CP294297	7LEAF--08
C 166	16	72.7	486	7	CF335999	JMT--07-B	CP286903	CR286903
C 167	16	72.7	487	7	CF337803	JMT--08-G	CP299626	7LEAF--03
C 168	16	72.7	488	7	CF335893	JMT--05-L	CP29884	7LEAF--02
C 169	16	72.7	490	7	CF294832	30DGS--04	CP337361	JMT--07-M
C 170	16	72.7	490	7	CF335453	JMT--05-C	CP332599	JMT--01-C



/cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="30DGSc-06-C24"  
 /tissue\_type="leaf"  
 /dev\_stage="30 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (30DGSc)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

**ORIGIN**

Query Match	72.7%	Score 16;	DB 7;	Length 200;
Best Local Matches	75.0%	Pred. No. 37;	Indels 0;	Gaps 0;
Matches 12;	Conservative	4; Mismatches 0;		

Qy 6 CUCACUGGAGCT 21  
 Db 107 CTCACTCGTGAGCTCT 92

**RESULT 3**

CF299826/c CF299826\_04-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-A01, mRNA sequence.

**DEFINITION**

Accession CF299826\_04-A01.g1 EST.

**LOCUS**

Organism Oryza sativa (japonica cultivar-group)

**DEFINITION**

Bukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.

**REFERENCE**

Authors Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., (bases 1 to 245)

**KEYWORDS**

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

**JOURNAL**

Title Large-scale Sequencing Analysis of Rice ESTs

**COMMENT**

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyonggi, Korea

Te: 82 31 330 6193

Fax: 82 31 322 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

**FEATURES source**

1.	.245	/organism="Oryza sativa (japonica cultivar-group)"
		/mol_type="mRNA"
		/cultivar="Nackdong"
		/db_xref="taxon:39947"
		/clone="7LEAF--04-A01.g1"
		/tissue_type="leaf"
		/dev_stage="7 days after germination"
		/lab_host="E.coli DH10B"
		/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
		/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

**ORIGIN**

Query Match	72.7%	Score 16;	DB 7;	Length 245;
Best Local Matches	75.0%	Pred. No. 37;	Mismatches 4;	Indels 0;
Matches 12;	Conservative			Gaps 0;

Qy 6 CUCACUGGAGCT 21  
 Db 133 CTCACTCGTGAGCTCT 118

**RESULT 5**

BE228712 BE228712\_04-A01.g1 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa (indica cultivar-group) cDNA clone 98AS3025, mRNA sequence.

**LOCUS**

**DEFINITION**

Accession BE228712\_04-A01.g1 EST.

**VERSION**

Organism Oryza sativa (indica cultivar-group)

**KEYWORDS**

Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.

**REFERENCE**

Authors Nahm, B.H., Kim, J.K., Cheong, P.J., Kim, M.J., Hahn, T.R., Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.

**JOURNAL**

Title Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)

**COMMENT**

Department of Cytogenetics National Inst. of Agri. Sci. and Tech, RDA Suwon, Kyunggi, Korea

**RESULT 4**

Query Match

Best Local Similarity 75.0%; Score 16; DB 7; Length 206;

Matches 12; Conservative 4; Indels 0; Gaps 0;

Qy 6 CUCACUGGAGCT 21  
 Db 106 CTCACTCGTGAGCTCT 91.

**ORIGIN**

FEATURES	source	Tel: 82 331 290 0301 Fax: 82 331 290 0307 Email: myeon@sunt0.asti.re.kr.	Qy	6 CUCACUCGUGAGCTT 21  :   :   :   : Db	129 CTCACCTCGTGAGCTT 114  :   :   : 6 CUCACUCGUGAGCTT 21  :   :   : EST 15-AUG-2003
Location/Qualifiers					
1..270					
/organism="Oryza sativa (indica cultivar-group)"					
/mol_type="mRNA"					
/db_xref="taxon:33946"					
/clone="198As3025"					
/tissue_type="Immature Seed"					
/dev_stage="5 days after pollination"					
/lab_host="E. coli SOR"					
/clone lib="Rice Immature Seed Lambda ZAPPII cDNA Library"					
/note="Vector: pBluescript SK(+); Site1: EcoRI; Site2: XbaI; directional cDNA library inserted into Lambda ZAPPII vector at 5' end with EcoRI and 3' end with Xba I site."					
ORIGIN					
Query Match		72.7%; Score 16; DB 2; Length 270;			
Best Local Similarity		75.0%; Pred. No. 37;			
Matches		12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;			
Qy	6 CUCACUCGUGAGCTT 21  :   :   :   : Db	32 CTCACCTCGTGAGCTT 47  :   :   : 6 CUCACUCGUGAGCTT 21  :   :   : EST 14-AUG-2003			
FEATURES	source				
6					
CP295034/c					
LOCUS		CP295034 -04-M16.g1 Rice leaf plasmid cDNA library I (30DGs) Oryza sativa (japonica cultivar-group) cDNA clone 30DGs--04-M16, mRNA sequence.			
DEFINITION					
ORGANISM		Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group)			
SOURCE		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzyeae; Orzya.			
VERSION		CP295034.1 GI:33664067			
KEYWORD					
EST.					
REFERENCE		Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.			
AUTHORS					
TITLE		Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL		Unpublished (2003)			
COMMENT		Contact: Nahm B.H.			
FEATURES	source				
6					
CP295034/c					
LOCUS		CP295034 -04-M16.g1 Rice leaf plasmid cDNA library I (30DGs) Oryza sativa (japonica cultivar-group) cDNA clone 30DGs--04-M16, mRNA sequence.			
DEFINITION					
ORGANISM		Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group)			
SOURCE		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzyeae; Orzya.			
VERSION		CP295034.1 GI:33664067			
KEYWORD					
EST.					
REFERENCE		Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.			
AUTHORS					
TITLE		Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL		Unpublished (2003)			
COMMENT		Contact: Nahm B.H.			
FEATURES	source				
6					
CP300491/c					
LOCUS		CP300491 -04-P09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-P09, mRNA sequence.			
DEFINITION					
ORGANISM		Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group)			
SOURCE		Bukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzyeae; Orzya.			
VERSION		CP300491.1 GI:33672252			
KEYWORD					
EST.					
REFERENCE		Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,			
AUTHORS					
ORIGIN					
Query Match		72.7%; Score 16; DB 7; Length 273;			
Best Local Similarity		75.0%; Pred. No. 37;			
Matches		12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;			
Qy	6 CUCACUCGUGAGCTT 21  :   :   : Db	182 CTCACCTCGTGAGCTT 167  :   :   : 6 CUCACUCGUGAGCTT 21  :   :   : EST 15-AUG-2003			
FEATURES	source				
6					
CP300491/c					
LOCUS		CP300491 -04-P09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-P09, mRNA sequence.			
DEFINITION					
ORGANISM		Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group)			
SOURCE		Bukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzyeae; Orzya.			
VERSION		CP300491.1 GI:33672252			
KEYWORD					
EST.					
REFERENCE		Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,			
AUTHORS					
ORIGIN					
Query Match		72.7%; Score 16; DB 7; Length 272;			
Best Local Similarity		75.0%; Pred. No. 37;			
Matches		12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;			



SOURCE	
ORGANISM	Oryza sativa (japonica cultivar-group)
	Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
Orzyace; Oryza.	
REFERENCE	1 (bases 1 to 281)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr.
FEATURES	
source	<p>1. .281 Location/Qualifiers</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nackdong"</p> <p>/db_xref="taxon:39947"</p> <p>/clone_id="7LEAF-01-PO9"</p> <p>/tissue_type="Leaf"</p> <p>/dev_stage="7 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"</p> <p>/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>
ORIGIN	
	<p>Query Match 72.7%; Score 16; DB 7; Length 281;</p> <p>Best Local Similarity 75.0%; Pred. No. 37;</p> <p>Matches 12; Conservative 4; Mismatches 0; Gaps 0;</p> <p>Db 115 CTCATCTGAGCTC 100</p>
RESULT	
12 CF294911/c	<p>283 bp mRNA linear EST 14-AUG-2003</p> <p>30DGs--04-J22.91 Rice leaf plasmid cDNA library I (30DGs) Oryza sativa (japonica cultivar-group) cDNA clone 30DGs--04-J22, mRNA sequence.</p>
DEFINITION	
	CF294911.1 GI:33663944
VERSION	
	EST
KEYWORDS	
ORGANISM	Oryza sativa (japonica cultivar-group)
	Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
Orzyace; Oryza.	
REFERENCE	1 (bases 1 to 283)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr.
FEATURES	
source	<p>1. .283 Location/Qualifiers</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/clone_id="Nackdong"</p>
ORIGIN	
	<p>Query Match 72.7%; Score 16; DB 7; Length 311;</p> <p>Best Local Similarity 75.0%; Pred. No. 37;</p> <p>Matches 12; Conservative 4; Mismatches 0; Gaps 0;</p> <p>Db 293 CTCATCGTGTGAGCTC 278</p>
RESULT	14 CB668058

LOCUS CB668085 DEFINITION 313 bp mRNA linear EST 09-APR-2003  
 Clone OSNED15M06.f OSJNED15M06.5 , mRNA sequence.  
 ACCESSION CB668085  
 VERSION 1 GI:29671810  
 KEYWORDS EST.  
 SOURCE ORGANISM Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group) Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE AUTHORS Jantsaburiyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,  
 Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.  
 TITLE Large-scale identification of ESTs involved in the interaction  
 between rice and Magnaporthe grisea  
 Unpublished (2003)  
 JOURNAL COMMENT Contact: Rod Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
 85721-0088, USA  
 Tel: 520 626 3967  
 Fax: 520 621 9288  
 Email: <http://genome.arizona.edu>  
 PCR Primers  
 FORWARD: gta aaa cga cgg cca gtg  
 BACKWARD: gta aac aca tat gag cat g  
 Plate: 15 row: M column: 06  
 Seq primer: gta aaa cga cgg cca gtg.  
 Location/Qualifiers 1..313  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nipponbare"  
 /db\_xref="Taxon:39947"  
 /clone="OSNED15M06"  
 /tissue\_type="Leaf"  
 /dev\_stage="3 week"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with Oligoribonucleotides and then used as templates for  
 RT-PCR."  
 FEATURES source  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, MyongJi University  
 Yongin, Kyunggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: [bhnahm@eggbio.com](mailto:bhnahm@eggbio.com), [bhnahm@bio.myongji.ac.kr](mailto:bhnahm@bio.myongji.ac.kr).  
 FEATURES source  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="Taxon:39947"  
 /clone="7LEAF--04-J16"  
 /tissue\_type="Leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with Oligoribonucleotides and then used as templates for  
 RT-PCR."  
 ORIGIN  
 RESULT 16  
 CF300267/C LOCUS 321 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--04-J16-g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--04-J16, mRNA  
 sequence.  
 ACCESSION CP300267  
 VERSION 1 GI:33672028  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group) Streptophyta; Embryophyta;  
 Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (bases 1 to 321)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, MyongJi University  
 Yongin, Kyunggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: [bhnahm@eggbio.com](mailto:bhnahm@eggbio.com), [bhnahm@bio.myongji.ac.kr](mailto:bhnahm@bio.myongji.ac.kr).  
 FEATURES source  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="Taxon:39947"  
 /clone="7LEAF--04-J16"  
 /tissue\_type="Leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with Oligoribonucleotides and then used as templates for  
 RT-PCR."  
 ORIGIN  
 RESULT 15  
 CF300735/C LOCUS 315 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--05-005\_g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--05-F05, mRNA  
 sequence.  
 ACCESSION CF300735  
 VERSION 1 GI:33672496  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group) Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)



/clone="30DGs--04-N22"  
 /tissue\_type="leaf"  
 /dev\_stage="30 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf Plasmid cDNA library I (30DGs)"  
 /note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."  
**ORIGIN**

Query Match	72.7%	Score 16;	DB 7;	Length 326;				
Best Local Similarity	75.0%	Pred. No.	37;					
Matches	12;	Conservative	4;	Mismatches	0;	Indels	0;	Gaps 0;

Qy 6 CUCACUGGAGCTCT 21  
 Db 308 CTCACCTCGAGCTCT 293

**RESULT 20**  
**LOCUS** CF300479\_c  
**DEFINITION** 326 bp mRNA linear EST 15-AUG-2003  
*7LEAF--04-017.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-017, mRNA sequence.*  
**ACCESSION** CF300479  
**VERSION** 1  
**KEYWORDS** EST.  
**ORGANISM** Oryza sativa (japonica cultivar-group)  
*Oryza sativa (japonica cultivar-group); Streptophytina; Embryophytina; Tracheophytina; Eukaryota; Viridiplantae; Liliopsida; Poaceae; Spermatophytina; Magnoliophytina; Streptophytina; Embryophytina; Tracheophytina; Ehrhartoidae; Oryzae; Oryza.*  
**REFERENCE** 1 (bases 1 to 326)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyunggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@gbio.com, bhnahn@bio.myongji.ac.kr.

**FEATURES source**

1.	329							
		/organism="Oryza sativa (japonica cultivar-group)"						
		/mol_type="mRNA"						
		/cultivar="Nackdong"						
		/db_xref="taxon:39947"						
		/clones="7LEAF--01-K01"						
		/tissue_type="leaf"						
		/dev_stage="7 days after germination"						
		/lab_host="E.coli DH10B"						
		/clone_lib="Rice leaf Plasmid cDNA library II (7LEAF)"						
		/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."						

**ORIGIN**

Query Match	72.7%	Score 16;	DB 7;	Length 329;				
Best Local Similarity	75.0%	Pred. No.	37;					
Matches	12;	Conservative	4;	Mismatches	0;	Indels	0;	Gaps 0;

Qy 6 CUCACUGGAGCTCT 21  
 Db 311 CTCACCTCGAGCTCT 296

**RESULT 22**  
**LOCUS** CF301705\_c  
**DEFINITION** 330 bp mRNA linear EST 15-AUG-2003  
*7LEAF--06-K17.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-K17, mRNA sequence.*  
**ACCESSION** CF301705  
**VERSION** 1  
**KEYWORDS** EST.  
**ORGANISM** Oryza sativa (japonica cultivar-group)  
*Oryza sativa (japonica cultivar-group); Streptophytina; Embryophytina; Tracheophytina; Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Ehrhartoidae; Oryzae; Oryza.*  
**REFERENCE** 1 (bases 1 to 330)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyunggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355

**RESULT 21**  
**LOCUS** CF3098299\_c  
**DEFINITION** 329 bp mRNA linear EST 15-AUG-2003

**FEATURES source**

1.	326							
		/organism="Oryza sativa (japonica cultivar-group)"						
		/mol_type="mRNA"						
		/cultivar="Nackdong"						
		/db_xref="taxon:39947"						
		/clones="7LEAF--04-O17"						
		/tissue_type="leaf"						
		/dev_stage="7 days after germination"						
		/lab_host="E.coli DH10B"						
		/clone_lib="Rice leaf Plasmid cDNA library II (7LEAF)"						
		/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."						

**ORIGIN**

Query Match	72.7%	Score 16;	DB 7;	Length 326;				
Best Local Similarity	75.0%	Pred. No.	37;					
Matches	12;	Conservative	4;	Mismatches	0;	Indels	0;	Gaps 0;

Qy 6 CUCACUGGAGCTCT 21  
 Db 308 CTCACCTCGAGCTCT 293

FEATURES source	Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr. 1. .330 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:39947" /clone="7LEAF-06-K17" /tissue_type="leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  ORIGIN	Db	105 CTCATCGTGAAGCTCT 90
RESULT 24 LOCUS CF294601/c DEFINITION 3DGGS-04-D07:g1 Rice leaf plasmid cDNA library I (3DGGS) Oryza sativa (japonica cultivar-group) cDNA clone 3DGGS--04-D07, mRNA sequence. ACCESSION CF294601 VERSION CF294601.1 KEYWORDS EST. SOURCE Oryza sativa (japonica cultivar-group) ORGANISM Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orzyeae; Orzya. REFERENCE 1 (bases 1 to 342) AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H. TITLE Large-scale Sequencing Analysis of Rice ESTs JOURNAL Unpublished (2003) COMMENT Contact: Nahm B.H. Genomics and Bioinformatics, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyunggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr. FEATURES source 1. .342 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="Taxon:39947" /clone="3DGGS-04-D07" /tissue_type="leaf" /dev_stage="30 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library I (3DGGS)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR." ORIGIN	Query Match 72.7%; Score 16; DB 7; Length 330; Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Qy 6 CUCACUGAGCUCT 21 Db 321 CTCATCGTGAAGCTCT 306	Query Match 72.7%; Score 16; DB 7; Length 342; Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Qy 6 CUCACUGAGCUCT 21 Db 324 CTCATCGTGAAGCTCT 309	
RESULT 23 LOCUS CF299101/c DEFINITION 7LEAF--02-P10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P10, mRNA sequence. ACCESSION CF299101 VERSION CF299101.1 KEYWORDS EST. SOURCE Oryza sativa (japonica cultivar-group) ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orzyeae; Orzya. REFERENCE 1 (bases 1 to 340) AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H. TITLE Large-scale Sequencing Analysis of Rice ESTs JOURNAL Unpublished (2003) COMMENT Contact: Nahm B.H. Genomics and Bioinformatics, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyunggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr. FEATURES source 1. .340 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:39947" /clone="7LEAF--02-P10" /tissue_type="leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR." ORIGIN	Query Match 72.7%; Score 16; DB 7; Length 340; Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Qy 6 CUCACUGAGCUCT 21	Query Match 72.7%; Score 16; DB 7; Length 343; Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Qy 6 CUCACUGAGCUCT 21	
RESULT 25 LOCUS CF300860/c DEFINITION 7LEAF-05-H23:g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-H23, mRNA sequence. ACCESSION CF300860 VERSION CF300860.1 KEYWORDS EST. SOURCE Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orzyeae; Orzya. REFERENCE 1 (bases 1 to 343) AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H. TITLE Large-scale Sequencing Analysis of Rice ESTs	Query Match 72.7%; Score 16; DB 7; Length 340; Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Qy 6 CUCACUGAGCUCT 21	Query Match 72.7%; Score 16; DB 7; Length 343; Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Qy 6 CUCACUGAGCUCT 21	

JOURNAL	Unpublished (2003)	COMMENT	Nahm, B.H.	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
FEATURES		source		
	1..343			/organism="Oryza sativa (japonica cultivar-group)"
				/mol_type="mRNA"
				/cultivar="Nackdong"
				/db_xref="taxon:39947"
				/clone="7LRF-05-H23"
				/tissue_type="leaf"
				/dev_stage="7 days after germination"
				/lab_host="E.coli DH10B"
				/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
				/note="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
		ORIGIN		
				Query Match 72.7%; Score 16; DB 7; Length 343;
				Best Local Similarity 75.0%; Pred. No. 37;
				Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
		Qy		6 CUCACUGGAGCT 21
		Db		:   :   :   :
				325 CTGACTCGTGAGCTCT 310
		RESULT	26	
		LOCUS	CF302308	349 bp mRNA linear EST 15-AUG-2003
		DEFINITION	7LEAF--07-L05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-L05, mRNA sequence.	
		ORGANISM	Oryza sativa (japonica cultivar-group)	
		ACCESSION	CF302308	
		VERSION	EST.	
		KEYWORDS		
		SOURCE	Oryza sativa (japonica cultivar-group)	
		ORGANISM	Oryza sativa (japonica cultivar-group)	
		REFERENCE		
		AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.	
		TITLE	Large-scale Sequencing Analysis of Rice ESTs	
		JOURNAL	Unpublished (2003)	
		COMMENT	Contact: Nahm, B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@gbbio.com, bhnahn@bio.myongji.ac.kr.	
		FEATURES		
		source		
			1..349	
			/organism="Oryza sativa (japonica cultivar-group)"	
			/mol_type="mRNA"	
			/cultivar="Nackdong"	
			/db_xref="taxon:39947"	
			/clone="7LRF-07-L05"	
			/tissue_type="leaf"	
			/dev_stage="7 days after germination"	
			/lab_host="E.coli DH10B"	
			/note="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."	
		ORIGIN		
				Query Match 72.7%; Score 16; DB 4; Length 350;
				Best Local Similarity 75.0%; Pred. No. 37;
				Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
		Qy		6 CUCACUGGAGCT 21
		Db		:   :   :   :
				11 CTGACTCGAGCTCT 26
		RESULT	28	
		LOCUS	CF333939/c	350 bp mRNA linear EST 18-AUG-2003
		DEFINITION	JMT--03-A17.91 AtUMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-A17, mRNA sequence.	
		ACCESSION	CF333939	
		VERSION	EST.	
		KEYWORDS		
		SOURCE	Oryza sativa (japonica cultivar-group)	
		ORGANISM	Oryza sativa (japonica cultivar-group)	
		REFERENCE		
		AUTHORS		
		TITLE		
		JOURNAL		
		COMMENT		
		FEATURES		
		source		
			1..349	
			/organism="Oryza sativa (japonica cultivar-group)"	
			/mol_type="mRNA"	
			/cultivar="Nackdong"	
			/db_xref="taxon:39947"	
			/clone="7LRF-07-L05"	
			/tissue_type="leaf"	
			/dev_stage="7 days after germination"	
			/lab_host="E.coli DH10B"	
			/note="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."	

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.K., and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6315  
Email: bhnahn@gpbi.com, bhnahn@bio.myongji.ac.kr.

FEATURES Source  
Location/Qualifiers  
1 .350  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:3947"  
/clone="03-A17"  
/tissue\_type="Leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone lib="AJM1-overexpressing transgenic rice plasmid  
CDNA Library (AJM1)"  
/note="Vector: PCR4-TOPO; site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasminolate Carboxyl methyltransferase overexpression line."

ORIGIN Query Match 72.7%; Score 16; DB 7; Length 350;  
Best Local Similarity 75.0%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUGGAGCUCT 21  
Db 323 CTCACTCGTAGCT 308

RESULT 29  
CF300157/C CF300157\_1 GI:33671918  
LOCUS EST  
DEFINITION 351 bp mRNA linear EST 15-AUG-2003  
Match 75.0% 70.91 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
activa (japonica cultivar-group) cDNA clone 7LEAF--04-H07, mRNA  
sequence.

ORGANISM  
ACCESION CF300157  
VERSION CF300157\_1  
KEYWORDS EST  
SOURCE  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Emberbatoidea; Oryzeae; Oryza.

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahn@gpbi.com, bhnahn@bio.myongji.ac.kr.

FEATURES Source  
Location/Qualifiers  
1 .351  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:3947"  
/clone="04-H07"  
/tissue\_type="leaf"

ORIGIN Query Match 72.7%; Score 16; DB 7; Length 352;  
Best Local Similarity 75.0%; Pred. No. 37;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUGGAGCUCT 21  
Db 334 CTCACTCGTAGCT 319

Search completed: July 21, 2005, 00:55:44  
Job time : 3094 secs

THIS PAGE IS BLANK

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:44:51 ; Search time 128 Seconds

(without alignments)  
 281.235 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaaucacucugagaggcuctt 22

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

## Post-processing: Listing first 300 summaries

Database : Issued\_Patents\_NA.\*

1: /cggn2\_6/predicta/1/ina/5A\_COMB.seq:\*
 2: /cggn2\_6/predicta/1/ina/5B\_COMB.seq:\*
 3: /cggn2\_6/predicta/1/ina/6A\_COMB.seq:\*
 4: /cggn2\_6/predicta/1/ina/6B\_COMB.seq:\*
 5: /cggn2\_6/predicta/1/ina/PCUTS\_COMB.seq:\*
 6: /cggn2\_6/predicta/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
c 1	15	68.2	234884	4	US-09-949-016-16420		Sequence 16420, A
c 2	14	63.6	348	3	US-09-134-001C-2127		Sequence 2127, Ap
c 3	14	63.6	428	4	US-09-210-767-8934		Sequence 8934, Ap
c 4	14	63.6	428	4	US-09-270-767-24276		Sequence 24276, A
c 5	14	63.6	3170	4	US-09-710-279-3849		Sequence 3849, Ap
c 6	14	63.6	4329	4	US-09-710-279-2051		Sequence 2051, Ap
c 7	14	63.6	300598	4	US-09-949-016-11868		Sequence 11868, A
c 8	14	63.6	302604	4	US-09-949-016-14588		Sequence 14588, A
c 9	14	63.6	304604	4	US-09-949-016-11589		Sequence 14589, A
c 10	14	63.6	308362	4	US-09-949-016-17119		Sequence 17119, A
c 11	14	63.6	4403765	3	US-09-103-840A-2		Sequence 2, Appl;
c 12	14	63.6	4411529	3	US-09-103-940A-1		Sequence 1, Appl;
c 13	13	59.1	240	4	US-09-88-039A-216		Sequence 216, App
c 14	13	59.1	601	4	US-09-949-016-22714		Sequence 27714, A
c 15	13	59.1	601	4	US-09-949-016-60781		Sequence 60781, A
c 16	13	59.1	601	4	US-09-949-016-60782		Sequence 60782, A
c 17	13	59.1	601	4	US-09-949-016-60783		Sequence 60783, A
c 18	13	59.1	601	4	US-09-949-016-60784		Sequence 60784, A
c 19	13	59.1	601	4	US-09-949-016-164641		Sequence 164641, Ap
c 20	13	59.1	1161	4	US-09-543-681A-3861		Sequence 3861, Ap
c 21	13	59.1	1411	4	US-09-549-016-60505		Sequence 505, Ap
c 22	13	59.1	1411	4	US-09-949-016-64615		Sequence 4615, Ap
c 23	13	59.1	1546	4	US-09-620-312D-452		Sequence 452, Ap
c 24	13	59.1	3250	3	US-09-521-0173-960		Sequence 960, App
c 25	13	59.1	3935	3	US-09-060-882-1		Sequence 1, Appl
c 26	13	59.1	4082	4	US-09-949-016-2772		Sequence 2722, Ap
c 27	13	59.1	6015	4	US-09-525-305-50		Sequence 50, Appl

Result No.	Score	Query	Match	Length	DB	ID	Description		
c 28	13	59.1	14205	4	US-09-949-016-14464		Sequence 14464, A		
c 29	13	59.1	14395	4	US-09-949-016-12247		Sequence 12247, A		
c 30	13	59.1	14395	4	US-09-949-016-16357		Sequence 16357, A		
c 31	13	59.1	26709	4	US-09-949-016-15720		Sequence 17520, A		
c 32	13	59.1	29598	3	US-09-341-587-6		Sequence 6, Appl		
c 33	13	59.1	42672	4	US-09-949-016-17253		Sequence 17253, A		
c 34	13	59.1	42672	4	US-09-949-016-17254		Sequence 17254, A		
c 35	13	59.1	68750	3	US-09-335-409-1		Sequence 1, Appl		
c 36	13	59.1	68750	3	US-09-568-102-1		Sequence 1, Appl		
c 37	13	59.1	68750	3	US-09-567-569-1		Sequence 1, Appl		
c 38	13	59.1	68750	3	US-09-558-480-1		Sequence 1, Appl		
c 39	13	59.1	68750	3	US-09-568-486-1		Sequence 1, Appl		
c 40	13	59.1	68750	3	US-09-568-472-1		Sequence 1, Appl		
c 41	13	59.1	68750	3	US-09-567-899-1		Sequence 1, Appl		
c 42	13	59.1	68750	3	US-09-557-884-1		Sequence 1, Appl		
c 43	13	59.1	75216	4	US-09-949-016-13369		Sequence 15369, A		
c 44	13	59.1	100928	4	US-09-949-016-14061		Sequence 14061, A		
c 45	13	59.1	117937	4	US-09-949-016-16926		Sequence 11926, A		
c 46	13	59.1	117937	4	US-09-949-016-18762		Sequence 12762, A		
c 47	13	59.1	283538	4	US-09-949-016-13506		Sequence 13506, A		
c 48	13	59.1	1830121	4	US-09-643-990A-1		Sequence 1, Appl		
c 49	13	59.1	1830121	4	US-09-026-320A-10		Sequence 10, Appl		
c 50	13	59.1	54.5	23	1	US-09-396-196G-72642		Patent No. 5496324	
c 51	12	54.5	24	6	5496924-50		Patent No. 5496324		
c 52	12	54.5	25	4	US-09-396-196G-72642		Sequence 52, Appl		
c 53	12	54.5	55	12	54.5	110	US-09-268-347-52	Sequence 52, Appl	
c 54	12	54.5	55	12	54.5	212	4	US-09-513-999C-19813	Sequence 19813, A
c 55	12	54.5	55	12	54.5	244	4	US-09-13-99C-365	Sequence 65, App
c 56	12	54.5	55	12	54.5	285	4	US-09-313-999A-1964	Sequence 1964, Ap
c 57	12	54.5	55	12	54.5	340	4	US-09-513-999C-2476	Sequence 2476, Ap
c 58	12	54.5	61	12	54.5	367	4	US-09-621-18415	Sequence 18415, A
c 59	12	54.5	61	12	54.5	371	4	US-09-513-999C-28424	Sequence 28424, Ap
c 60	12	54.5	61	12	54.5	446	4	US-09-621-976-10841	Sequence 10841, A
c 61	12	54.5	61	12	54.5	466	4	US-09-621-18219	Sequence 18219, A
c 62	12	54.5	61	12	54.5	510	4	US-09-322B-352-3457	Sequence 3457, Ap
c 63	12	54.5	61	12	54.5	536	3	US-09-615-192A-225	Sequence 225, App
c 64	12	54.5	67	12	54.5	545	3	US-09-998-16-122	Sequence 122, App
c 65	12	54.5	68	12	54.5	601	4	US-09-949-016-34423	Sequence 23423, A
c 66	12	54.5	69	12	54.5	601	4	US-09-949-016-29772	Sequence 19772, A
c 67	12	54.5	70	12	54.5	601	4	US-09-949-016-10889	Sequence 30889, A
c 68	12	54.5	71	12	54.5	601	4	US-09-949-016-33980	Sequence 33980, A
c 69	12	54.5	72	12	54.5	601	4	US-09-949-016-33981	Sequence 33981, A
c 70	12	54.5	73	12	54.5	601	4	US-09-949-016-39068	Sequence 39068, A
c 71	12	54.5	74	12	54.5	601	4	US-09-949-016-48740	Sequence 48740, A
c 72	12	54.5	75	12	54.5	601	4	US-09-949-016-66284	Sequence 66284, A
c 73	12	54.5	76	12	54.5	601	4	US-09-949-016-88078	Sequence 88078, A
c 74	12	54.5	77	12	54.5	601	4	US-09-949-016-88079	Sequence 88079, A
c 75	12	54.5	78	12	54.5	601	4	US-09-949-016-105259	Sequence 105259,
c 76	12	54.5	79	12	54.5	601	4	US-09-949-016-1845	Sequence 121845,
c 77	12	54.5	80	12	54.5	601	4	US-09-949-016-13334	Sequence 13334, A
c 78	12	54.5	81	12	54.5	601	4	US-09-949-016-134957	Sequence 134957,
c 79	12	54.5	82	12	54.5	601	4	US-09-949-016-16879	Sequence 146879,
c 80	12	54.5	83	12	54.5	601	4	US-09-949-016-162011	Sequence 162011,
c 81	12	54.5	84	12	54.5	601	4	US-09-949-016-162013	Sequence 162013,
c 82	12	54.5	85	12	54.5	601	4	US-09-949-016-162014	Sequence 162014,
c 83	12	54.5	86	12	54.5	601	4	US-09-949-016-164031	Sequence 146031,
c 84	12	54.5	87	12	54.5	601	4	US-09-949-016-16299	Sequence 146299,
c 85	12	54.5	88	12	54.5	601	4	US-09-949-016-164246	Sequence 182426,
c 86	12	54.5	89	12	54.5	601	4	US-09-949-016-183700	Sequence 183700,
c 87	12	54.5	90	12	54.5	601	4	US-09-949-016-183893	Sequence 183893,
c 88	12	54.5	91	12	54.5	601	4	US-09-949-016-187991	Sequence 187991,
c 89	12	54.5	92	12	54.5	601	4	US-09-949-016-19215	Sequence 199215,
c 90	12	54.5	93	12	54.5	601	4	US-09-949-016-19216	Sequence 199216,
c 91	12	54.5	94	12	54.5	601	4	US-09-949-016-1119	Sequence 119, App
c 92	12	54.5	95	12	54.5	601	4	US-09-949-016-187991	Sequence 5322, App

Sequence 1, Appli	1	Appli
Sequence 2, Appli	2	US-08-686-417-1
Sequence 3, Appli	3	US-09-128-352-3329
Sequence 4, Appli	4	US-08-904-284-1
Sequence 5, Appli	5	US-09-189-039A-6813
Sequence 6, Appli	6	US-09-328-A-1546
Sequence 7, Appli	7	US-09-602-777A-111
Sequence 8, Appli	8	US-09-513-681A-2202
Sequence 9, Appli	9	US-09-118-442-29
Sequence 10, Appli	10	US-09-302-622B-105
Sequence 11, Appli	11	US-09-912-161-45
Sequence 12, Appli	12	US-08-95-693B-27
Sequence 13, Appli	13	PCT-US94-14436-27
Sequence 14, Appli	14	US-08-588-983-1
Sequence 15, Appli	15	US-08-976-1
Sequence 16, Appli	16	US-08-588-976-1
Sequence 17, Appli	17	US-08-724-334A-14
Sequence 18, Appli	18	US-09-302-622B-105
Sequence 19, Appli	19	US-09-677-064-29
Sequence 20, Appli	20	US-08-95-693B-27
Sequence 21, Appli	21	US-09-911-781-23
Sequence 22, Appli	22	US-10-400-90-23
Sequence 23, Appli	23	US-08-588-983-1
Sequence 24, Appli	24	US-09-949-016-3155
Sequence 25, Appli	25	US-09-949-016-3241
Sequence 26, Appli	26	US-09-949-016-3245-10
Sequence 27, Appli	27	US-08-663-566A-10
Sequence 28, Appli	28	US-08-923-610-10
Sequence 29, Appli	29	US-08-288-068A-10
Sequence 30, Appli	30	US-08-362-210A-10
Sequence 31, Appli	31	US-08-804-372A-8
Sequence 32, Appli	32	US-08-097-552A-29
Sequence 33, Appli	33	US-08-180-640A-29
Sequence 34, Appli	34	US-08-295-80-29
Sequence 35, Appli	35	US-08-188-237A-29
Sequence 36, Appli	36	US-08-315-992A-29
Sequence 37, Appli	37	US-08-820-15A-29
Sequence 38, Appli	38	US-08-097-552A-29
Sequence 39, Appli	39	US-09-667-135-3
Sequence 40, Appli	40	US-09-949-016-3156
Sequence 41, Appli	41	US-09-949-016-3242
Sequence 42, Appli	42	US-08-820-210A-10
Sequence 43, Appli	43	US-08-362-210A-10
Sequence 44, Appli	44	US-08-804-372A-8
Sequence 45, Appli	45	US-09-949-016-3155
Sequence 46, Appli	46	US-09-949-016-3241
Sequence 47, Appli	47	US-08-180-640A-29
Sequence 48, Appli	48	US-08-295-80-29
Sequence 49, Appli	49	US-08-188-237A-29
Sequence 50, Appli	50	US-08-315-992A-29
Sequence 51, Appli	51	US-08-820-15A-29
Sequence 52, Appli	52	US-08-097-552A-29
Sequence 53, Appli	53	US-09-667-135-3
Sequence 54, Appli	54	US-09-949-016-3156
Sequence 55, Appli	55	US-09-949-016-3242
Sequence 56, Appli	56	US-08-820-210A-10
Sequence 57, Appli	57	US-08-362-210A-10
Sequence 58, Appli	58	US-09-949-016-3155
Sequence 59, Appli	59	US-09-949-016-3241
Sequence 60, Appli	60	US-08-180-640A-29
Sequence 61, Appli	61	US-08-295-80-29
Sequence 62, Appli	62	US-08-188-237A-29
Sequence 63, Appli	63	US-08-315-992A-29
Sequence 64, Appli	64	US-08-820-15A-29
Sequence 65, Appli	65	US-08-097-552A-29
Sequence 66, Appli	66	US-09-667-135-3
Sequence 67, Appli	67	US-09-949-016-3156
Sequence 68, Appli	68	US-09-949-016-3242
Sequence 69, Appli	69	US-08-820-210A-10
Sequence 70, Appli	70	US-08-362-210A-10
Sequence 71, Appli	71	US-09-949-016-3155
Sequence 72, Appli	72	US-09-949-016-3241
Sequence 73, Appli	73	US-08-180-640A-29
Sequence 74, Appli	74	US-08-295-80-29
Sequence 75, Appli	75	US-08-188-237A-29
Sequence 76, Appli	76	US-08-315-992A-29
Sequence 77, Appli	77	US-08-820-15A-29
Sequence 78, Appli	78	US-08-097-552A-29
Sequence 79, Appli	79	US-09-667-135-3
Sequence 80, Appli	80	US-09-949-016-3156
Sequence 81, Appli	81	US-09-949-016-3242
Sequence 82, Appli	82	US-08-820-210A-10
Sequence 83, Appli	83	US-08-362-210A-10
Sequence 84, Appli	84	US-09-949-016-3155
Sequence 85, Appli	85	US-09-949-016-3241
Sequence 86, Appli	86	US-08-180-640A-29
Sequence 87, Appli	87	US-08-295-80-29
Sequence 88, Appli	88	US-08-188-237A-29
Sequence 89, Appli	89	US-08-315-992A-29
Sequence 90, Appli	90	US-08-820-15A-29
Sequence 91, Appli	91	US-08-097-552A-29
Sequence 92, Appli	92	US-09-667-135-3
Sequence 93, Appli	93	US-09-949-016-3156
Sequence 94, Appli	94	US-09-949-016-3242
Sequence 95, Appli	95	US-08-820-210A-10
Sequence 96, Appli	96	US-08-362-210A-10
Sequence 97, Appli	97	US-09-949-016-3155
Sequence 98, Appli	98	US-09-949-016-3241
Sequence 99, Appli	99	US-08-180-640A-29
Sequence 100, Appli	100	US-08-295-80-29
Sequence 101, Appli	101	US-08-188-237A-29
Sequence 102, Appli	102	US-08-315-992A-29
Sequence 103, Appli	103	US-08-820-15A-29
Sequence 104, Appli	104	US-08-097-552A-29
Sequence 105, Appli	105	US-09-667-135-3
Sequence 106, Appli	106	US-09-949-016-3156
Sequence 107, Appli	107	US-09-949-016-3242
Sequence 108, Appli	108	US-08-820-210A-10
Sequence 109, Appli	109	US-08-362-210A-10
Sequence 110, Appli	110	US-09-949-016-3155
Sequence 111, Appli	111	US-09-949-016-3241
Sequence 112, Appli	112	US-08-180-640A-29
Sequence 113, Appli	113	US-08-295-80-29
Sequence 114, Appli	114	US-08-188-237A-29
Sequence 115, Appli	115	US-08-315-992A-29
Sequence 116, Appli	116	US-08-820-15A-29
Sequence 117, Appli	117	US-08-097-552A-29
Sequence 118, Appli	118	US-09-667-135-3
Sequence 119, Appli	119	US-09-949-016-3156
Sequence 120, Appli	120	US-09-949-016-3242
Sequence 121, Appli	121	US-08-820-210A-10
Sequence 122, Appli	122	US-08-362-210A-10
Sequence 123, Appli	123	US-09-949-016-3155
Sequence 124, Appli	124	US-09-949-016-3241
Sequence 125, Appli	125	US-08-180-640A-29
Sequence 126, Appli	126	US-08-295-80-29
Sequence 127, Appli	127	US-08-188-237A-29
Sequence 128, Appli	128	US-08-315-992A-29
Sequence 129, Appli	129	US-08-820-15A-29
Sequence 130, Appli	130	US-08-097-552A-29
Sequence 131, Appli	131	US-09-667-135-3
Sequence 132, Appli	132	US-09-949-016-3156
Sequence 133, Appli	133	US-09-949-016-3242
Sequence 134, Appli	134	US-08-820-210A-10
Sequence 135, Appli	135	US-08-362-210A-10
Sequence 136, Appli	136	US-09-949-016-3155
Sequence 137, Appli	137	US-09-949-016-3241
Sequence 138, Appli	138	US-08-180-640A-29
Sequence 139, Appli	139	US-08-295-80-29
Sequence 140, Appli	140	US-08-188-237A-29
Sequence 141, Appli	141	US-08-315-992A-29
Sequence 142, Appli	142	US-08-820-15A-29
Sequence 143, Appli	143	US-08-097-552A-29
Sequence 144, Appli	144	US-09-667-135-3
Sequence 145, Appli	145	US-09-949-016-3156
Sequence 146, Appli	146	US-09-949-016-3242
Sequence 147, Appli	147	US-08-820-210A-10
Sequence 148, Appli	148	US-08-362-210A-10
Sequence 149, Appli	149	US-09-949-016-3155
Sequence 150, Appli	150	US-09-949-016-3241
Sequence 151, Appli	151	US-08-180-640A-29
Sequence 152, Appli	152	US-08-295-80-29
Sequence 153, Appli	153	US-08-188-237A-29
Sequence 154, Appli	154	US-08-315-992A-29
Sequence 155, Appli	155	US-08-820-15A-29
Sequence 156, Appli	156	US-08-097-552A-29
Sequence 157, Appli	157	US-09-667-135-3
Sequence 158, Appli	158	US-09-949-016-3156
Sequence 159, Appli	159	US-09-949-016-3242
Sequence 160, Appli	160	US-08-820-210A-10
Sequence 161, Appli	161	US-08-362-210A-10
Sequence 162, Appli	162	US-09-949-016-3155
Sequence 163, Appli	163	US-09-949-016-3241
Sequence 164, Appli	164	US-08-180-640A-29
Sequence 165, Appli	165	US-08-295-80-29
Sequence 166, Appli	166	US-08-188-237A-29
Sequence 167, Appli	167	US-08-315-992A-29
Sequence 168, Appli	168	US-08-820-15A-29
Sequence 169, Appli	169	US-08-097-552A-29
Sequence 170, Appli	170	US-09-667-135-3
Sequence 171, Appli	171	US-09-949-016-3156
Sequence 172, Appli	172	US-09-949-016-3242
Sequence 173, Appli	173	US-08-820-210A-10
Sequence 174, Appli	174	US-08-362-210A-10
Sequence 175, Appli	175	US-09-949-016-3155
Sequence 176, Appli	176	US-09-949-016-3241
Sequence 177, Appli	177	US-08-180-640A-29
Sequence 178, Appli	178	US-08-295-80-29
Sequence 179, Appli	179	US-08-188-237A-29
Sequence 180, Appli	180	US-08-315-992A-29
Sequence 181, Appli	181	US-08-820-15A-29
Sequence 182, Appli	182	US-08-097-552A-29
Sequence 183, Appli	183	US-09-667-135-3
Sequence 184, Appli	184	US-09-949-016-3156
Sequence 185, Appli	185	US-09-949-016-3242
Sequence 186, Appli	186	US-08-820-210A-10
Sequence 187, Appli	187	US-08-362-210A-10
Sequence 188, Appli	188	US-09-949-016-3155
Sequence 189, Appli	189	US-09-949-016-3241
Sequence 190, Appli	190	US-08-180-640A-29
Sequence 191, Appli	191	US-08-295-80-29
Sequence 192, Appli	192	US-08-188-237A-29
Sequence 193, Appli	193	US-08-315-992A-29
Sequence 194, Appli	194	US-08-820-15A-29
Sequence 195, Appli	195	US-08-097-552A-29
Sequence 196, Appli	196	US-09-667-135-3
Sequence 197, Appli	197	US-09-949-016-3156
Sequence 198, Appli	198	US-09-949-016-3242
Sequence 199, Appli	199	US-08-820-210A-10
Sequence 200, Appli	200	US-08-362-210A-10
Sequence 201, Appli	201	US-09-949-016-3155
Sequence 202, Appli	202	US-09-949-016-3241
Sequence 203, Appli	203	US-08-180-640A-29
Sequence 204, Appli	204	US-08-295-80-29
Sequence 205, Appli	205	US-08-188-237A-29
Sequence 206, Appli	206	US-08-315-992A-29
Sequence 207, Appli	207	US-08-820-15A-29
Sequence 208, Appli	208	US-08-097-552A-29
Sequence 209, Appli	209	US-09-667-135-3
Sequence 210, Appli	210	US-09-949-016-3156
Sequence 211, Appli	211	US-09-949-016-3242
Sequence 212, Appli	212	US-08-820-210A-10
Sequence 213, Appli	213	US-08-362-210A-10
Sequence 214, Appli	214	US-09-949-016-3155
Sequence 215, Appli	215	US-09-949-016-3241
Sequence 216, Appli	216	US-08-180-640A-29
Sequence 217, Appli	217	US-08-295-80-29
Sequence 218, Appli	218	US-08-188-237A-29
Sequence 219, Appli	219	US-08-315-992A-29
Sequence 220, Appli	220	US-08-820-15A-29
Sequence 221, Appli	221	US-08-097-552A-29
Sequence 222, Appli	222	US-09-667-135-3
Sequence 223, Appli	223	US-09-949-016-3156
Sequence 224, Appli	224	US-09-949-016-3242
Sequence 225, Appli	225	US-08-820-210A-10
Sequence 226, Appli	226	US-08-362-210A-10
Sequence 227, Appli	227	US-09-949-016-3155
Sequence 228, Appli	228	US-09-949-016-3241
Sequence 229, Appli	229	US-08-180-640A-29
Sequence 230, Appli	230	US-08-295-80-29
Sequence 231, Appli	231	US-08-188-237A-29
Sequence 232, Appli	232	US-08-315-992A-29
Sequence 233, Appli	233	US-08-820-15A-29
Sequence 234, Appli	234	US-08-097-552A-29
Sequence 235, Appli	235	US-09-667-135-3
Sequence 236, Appli	236	US-09-949-016-3156
Sequence 237, Appli	237	US-09-949-016-3242
Sequence 238, Appli	238	US-08-820-210A-10
Sequence 239, Appli	239	US-08-362-210A-10
Sequence 240, Appli	240	US-09-949-016-3155
Sequence 241, Appli	241	US-09-949-016-3241
Sequence 242, Appli	242	US-08-180-640A-29
Sequence 243, Appli	243	US-08-295-80-29
Sequence 244, Appli	244	US-08-188-237A-29
Sequence 245, Appli	245	US-08-315-992A-29
Sequence 246, Appli	246	US-08-820-210A-10
Sequence 247, Appli	247	US-08-362-210A-10
Sequence 248, Appli	248	US-09-949-016-3155
Sequence 249, Appli	249	US-09-949-016-3241
Sequence 250, Appli	250	US-08-180-640A-29
Sequence 251, Appli	251	US-08-295-80-29
Sequence 252, Appli	252	US-08-188-237A-29
Sequence 253, Appli	253	US-08-315-992A-29
Sequence 254, Appli	254	US-08-820-210A-10
Sequence 255, Appli	255	US-08-362-210A-10
Sequence 256, Appli	256	US-09-949-016-3155
Sequence 257, Appli	257	US-09-949-016-3241
Sequence 258, Appli	258	US-08-180-640A-29
Sequence 259, Appli	259	US-08-295-80-29
Sequence 260, Appli	260	US-08-188-237A-29
Sequence 261, Appli	261	US-08-315-992A-29
Sequence 262, Appli	262	US-08-820-210A-10
Sequence 263, Appli	263	US-08-362-210A-10
Sequence 264, Appli	264	US-09-949-016-3155
Sequence 265, Appli	265	US-09-949-016-3241
Sequence 266, Appli	266	US-08-180-640A-29
Sequence 267, Appli	267	US-08-295-80-29
Sequence 268, Appli	268	US-08-188-237A-29
Sequence 269, Appli	269	US-08-315-992A-29
Sequence 270, Appli	270	US-08-820

**RESULT 1**

; PRIORITY INFORMATION:  
; Sequence 16420/c  
; Application US/09949016  
; Patent No. 6812319  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

**RESULT 2**

; PRIORITY INFORMATION:  
; Sequence 16420/c  
; Application US/09949016  
; Patent No. 6812319  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768

Sequence 15065, A-  
Sequence 17016, A-  
Sequence 17246, A-  
Sequence 11965, A-  
Sequence 11965, A-  
Sequence 1, Appli-  
Sequence 1, Appli-  
Sequence 12824, A-  
Sequence 14832, A-  
Sequence 14833, A-  
Sequence 14833, A-  
Sequence 17108, A-  
Sequence 17109, A-  
Sequence 15836, A-  
Sequence 12144, A-  
Sequence 13526, A-  
Sequence 30, Appli-  
Sequence 13184, A-  
Sequence 12007, A-  
Sequence 16781, A-  
Sequence 16502, A-  
Sequence 16512, A-  
Sequence 17272, A-  
Sequence 16851, A-  
Sequence 14186, A-  
Sequence 15200, A-  
Sequence 12360, A-  
Sequence 15781, A-  
Sequence 12114, A-  
Sequence 160370,  
; Sequence 2127, Application US/09134001C  
; CURRENT APPLICATION NUMBER: US/09/134-001C-2127  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134-001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5574  
; SEQ ID NO 2127  
; LENGTH: 348  
; ORGANISM: *Staphylococcus epidermidis*  
; Sequence 17011, A-  
Sequence 12564, A-  
Sequence 13694, A-  
Sequence 12245, A-  
Sequence 13214, A-  
Sequence 14928, A-  
Sequence 17011, A-  
Sequence 11800, A-  
Sequence 14926, A-  
Sequence 14927, A-  
Sequence 17362, A-  
Sequence 14928, A-  
Sequence 13693, A-  
Sequence 12474, A-  
Sequence 15402, A-  
Sequence 16319, A-  
Sequence 13032, A-  
Sequence 13807, A-  
Sequence 13694, A-  
Sequence 15414, A-  
Sequence 15494, A-  
Sequence 15494, A-

## ALIGNMENTS

**RESULT 3**

; Sequence 8994, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-054  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8994  
; LENGTH: 428  
; TYPE: DNA  
; ORGANISM: *Drosophila melanogaster*  
; Sequence 14794, A-  
; Sequence 142504, A-  
; Sequence 142505, A-  
; Sequence 152070, A-  
; Sequence 153866, A-  
; Sequence 165651, A-  
; Sequence 168971, A-  
; Sequence 183202, A-  
; Sequence 183770, A-  
; Sequence 183770, A-

**RESULT 4**

; Sequence 8994, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-054  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8994  
; LENGTH: 428  
; TYPE: DNA  
; ORGANISM: *Drosophila melanogaster*  
; Sequence 14794, A-  
; Sequence 142504, A-  
; Sequence 142505, A-  
; Sequence 152070, A-  
; Sequence 153866, A-  
; Sequence 165651, A-  
; Sequence 168971, A-  
; Sequence 183202, A-  
; Sequence 183770, A-  
; Sequence 183770, A-

; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PUS480US  
 ; CURRENT APPLICATION NUMBER: US/09/710,279  
 ; CURRENT FILING DATE: 2000-11-09  
 ; PRIOR APPLICATION NUMBER: 60/164,258  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 2051  
 ; LENGTH: 4329  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: nucleic acid sequence  
 ; US-09-710-279-2051  
 Qy 7 UCACUGGAGCU 20  
 Db 356 TCACTCGGAGTC 369  
**RESULT 4**  
 US-09-270-767-24276  
 ; Sequence 24276, Application US/09270767  
 ; Patent No. 670491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Honburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 24276  
 ; LENGTH: 428  
 ; TYPE: DNA  
 ; ORGANISM: *Drosophila melanogaster*  
 ; US-09-270-767-24276  
 Query Match 63.6%; Score 14; DB 4; Length 428;  
 Best Local Similarity 71.4%; Pred. No. 26;  
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 UCACUGGAGCU 20  
 Db 356 TCACTCGGAGTC 369  
**RESULT 5**  
 US-09-710-279-3849  
 ; Sequence 3849, Application US/09710279  
 ; Patent No. 70492  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMMERLY, WILLIAM JOHN  
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 ; FILE REFERENCE: PUS480US  
 ; CURRENT APPLICATION NUMBER: US/09/710,279  
 ; CURRENT FILING DATE: 2000-11-09  
 ; PRIOR APPLICATION NUMBER: 60/164,258  
 ; PRIOR FILING DATE: 1999-11-09  
 ; NUMBER OF SEQ ID NOS: 4472  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 3849  
 ; LENGTH: 170  
 ; TYPE: DNA  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: nucleic acid sequence  
 ; US-09-710-279-3849  
 Query Match 63.6%; Score 14; DB 4; Length 3170;  
 Best Local Similarity 71.4%; Pred. No. 24;  
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GUGAACUACUGU 14  
 Db 1090 GTGAACTCACTCGT 1103  
**RESULT 6**  
 US-09-710-279-2051  
 ; Sequence 2051, Application US/09710279  
 ; Patent No. 6703492  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; US-09-710-2051  
 Query Match 63.6%; Score 14; DB 4; Length 4329;  
 Best Local Similarity 71.4%; Pred. No. 24;  
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GUGAACUACUGU 14  
 Db 101 GTGAACTCACTCGT 114  
**RESULT 7**  
 US-09-949-016-11868/C  
 ; Sequence 11868, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 11868  
 ; LENGTH: 300598  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(300598)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-949-016-11868  
 Query Match 63.6%; Score 14; DB 4; Length 300598;  
 Best Local Similarity 78.6%; Pred. No. 21;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 ACTUCGUAGGUCUTT 22  
 Db 93184 ACTCGTGAGCTCTT 93171  
**RESULT 8**  
 US-09-949-016-14588/C  
 ; Sequence 14588, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```

FILE REFERENCE: CLO01307 ; APPLICANT: VENTER, J. Craig et al.
; CURRENT APPLICATION NUMBER: US/09/949,016 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; CURRENT FILING DATE: 2000-04-14 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; PRIORITY NUMBER: 60/241,755 ; FILE REFERENCE: CLO01307
; PRIOR APPLICATION NUMBER: 60/241,755 ; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14 ; CURRENT FILING DATE: 2000-04-14
; PRIORITY NUMBER: 60/237,768 ; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03 ; PRIOR FILING DATE: 2000-10-20
; PRIORITY NUMBER: 60/231,498 ; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08 ; PRIOR FILING DATE: 2000-10-03
; PRIORITY NUMBER: 60/231,498 ; PRIORITY APPLICATION NUMBER: 60/231,498
; SEQ ID NO: 14588 ; NUMBER OF SEQ ID NOS: 207012
; LENGTH: 302604 ; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: DNA ; SOFTWARE: FastSEQ for Windows Version 4.0
; ORGANISM: Human ; SEQ ID NO: 17119
; FEATURE: NAME/KEY: misc_feature ; LENGTH: 308362
; LOCATION: (1)...(308364) ; TYPE: DNA
; OTHER INFORMATION: n = A,T,C or G ; ORGANISM: Human
; US-09-949-016-14588 ; FEATURE: NAME/KEY: misc_feature
; QUERY MATCHES: 9 ACUCUGAGACUCTT 22 ; LOCATION: (1)...(308362)
; DB 143190 ACTCTGAGCTCTT 143177 ; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-14589/C ; QUERY MATCHES: 9 ACUCUGAGACUCTT 22
; SEQUENCE 14509, Application US/09949016 ; DB 143006 ACTCTGAGCTCTT 142993
; PARENT NO. 6812339 ; RESULT 11
; GENERAL INFORMATION: ; US-09-103-840A-2/C
; APPLICANT: VENTER, J. Craig et al. ; Sequence 2, Application US/09103840A
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; PARENT NO. 6294318
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF ; GENERAL INFORMATION:
; FILE REFERENCE: CLO01307 ; APPLICANT: FLEISCHMAN, Robert D.
; CURRENT APPLICATION NUMBER: US/09/949,016 ; APPLICANT: WHITE, Owen R.
; CURRENT FILING DATE: 2000-04-14 ; APPLICANT: FRASER, Claire M.
; PRIOR APPLICATION NUMBER: 60/241,755 ; APPLICANT: VENTER, John C.
; PRIOR FILING DATE: 2000-10-20 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; PRIORITY NUMBER: 60/237,768 ; FILE REFERENCE: 24366-20007.00
; PRIOR FILING DATE: 2000-10-03 ; CURRENT APPLICATION NUMBER: US/09/103,840A
; PRIORITY NUMBER: 60/231,498 ; CURRENT FILING DATE: 1998-06-24
; PRIOR FILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 2
; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: PatentIn Ver. 2.1
; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 2
; LENGTH: 302604 ; LENGTH: 4403765
; TYPE: DNA ; ORGANISM: Mycobacterium tuberculosis
; ORGANISM: Human ; FEATURE: NAME/KEY: misc_feature
; FEATURE: LOCATION: (1)...(302604) ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: n = A,T,C or G ; US-09-103-840A-2
; US-09-949-016-14589 ; QUERY MATCHES: 9 ACUCUGAGACUCTT 22
; QUERY MATCHES: 9 ACUCUGAGACUCTT 22 ; PARENT NO. 6294318
; DB 143190 ACTCTGAGCTCTT 143177 ; GENERAL INFORMATION:
; DB 143006 ACTCTGAGCTCTT 142993 ; RESULT 12
; US-09-949-016-17119/C ; Sequence 17119, Application US/09949016
; PARENT NO. 6812339 ; PARENT NO. 6294318
; GENERAL INFORMATION: ; GENERAL INFORMATION:

```

```

; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          63.6%;  Score 14;  DB 3;  Length 4411529;
Best Local Similarity 71.4%;  Pred. No. 18;  Matches 10;  Conservative 4;  Indels 0;  Gaps 0;
Matches 10;  Conservative 4;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 13
US-09-489-039A-216
; Sequence 216, Application US/09489039A
; Patent No. 661036
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-216

Query Match          59.1%;  Score 13;  DB 4;  Length 240;
Best Local Similarity 76.9%;  Pred. No. 1.1e+02;  Matches 10;  Conservative 3;  Indels 0;  Gaps 0;
Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 14
US-09-949-016-27714
; Sequence 27714, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60781
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27714

Query Match          59.1%;  Score 13;  DB 4;  Length 601;
Best Local Similarity 76.9%;  Pred. No. 1e+02;  Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 15
US-09-949-016-60781/C
; Sequence 60781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60782
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60781/C

Query Match          59.1%;  Score 13;  DB 4;  Length 601;
Best Local Similarity 76.9%;  Pred. No. 1e+02;  Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 16
US-09-949-016-60782/C
; Sequence 60782, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60782
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60782/C

Query Match          59.1%;  Score 13;  DB 4;  Length 601;
Best Local Similarity 76.9%;  Pred. No. 1e+02;  Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

RESULT 17
US-09-949-016-60783/C
; Sequence 60783, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60783
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60783/C

Query Match          59.1%;  Score 13;  DB 4;  Length 601;
Best Local Similarity 76.9%;  Pred. No. 1e+02;  Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

```

Organism: Human  
US-09-949-016-60782

Query Match 59.1%; Score 13; DB 4; Length 601;  
Best Local Similarity 76.9%; Pred. No. 1e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0;  
Gaps 0;

Qy 1 GUGAACUACUCG 13  
Db 339 GTGAACTCACTCG 327

RESULT 17  
US-09-949-016-60783/C  
; Sequence 60783, Application US/09949016

GENERAL INFORMATION:  
; Patent No. 6812339

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 60783  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-60783

Query Match 59.1%; Score 13; DB 4; Length 601;  
Best Local Similarity 76.9%; Pred. No. 1e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0;  
Gaps 0;

Qy 1 GUGAACUACUCG 13  
Db 332 GTGAACTCACTCG 320

RESULT 18  
US-09-949-016-60784/C  
; Sequence 60784, Application US/09949016

GENERAL INFORMATION:  
; Patent No. 6812339

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 60784  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-60784

Query Match 59.1%; Score 13; DB 4; Length 601;  
Best Local Similarity 76.9%; Pred. No. 1e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0;  
Gaps 0;

Qy 1 GUGAACUACUCG 13  
Db 233 GTGAACTCACTCG 221

RESULT 19  
US-09-94-016-164641  
; Sequence 164641, Application US/09949016

GENERAL INFORMATION:  
; Patent No. 6812339

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 164641  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-94-016-164641

Query Match 59.1%; Score 13; DB 4; Length 601;  
Best Local Similarity 76.9%; Pred. No. 1e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0;  
Gaps 0;

Qy 4 AACUACUCCUGA 16  
Db 238 AACUACUCCGTGA 250

RESULT 20  
US-09-54-681A-3861  
; Sequence 3861, Application US/09543681A

GENERAL INFORMATION:  
; Patent No. 6605709

APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A.  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO: 3861  
LENGTH: 1161  
TYPE: DNA  
ORGANISM: Proteus mirabilis  
US-09-54-681A-3861

Query Match 59.1%; Score 13; DB 4; Length 1161;  
Best Local Similarity 69.2%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 0; Indels 0;  
Gaps 0;

Qy 7 UCACUCGGAGCU 19  
Db 170 TCACUTGTCAGCT 182

RESULT 21  
US-09-94-016-505  
; Sequence 505, Application US/09949016

Query Match 59.1%; Score 13; DB 4; Length 601;  
Best Local Similarity 76.9%; Pred. No. 1e+02;

Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 505  
LENGTH: 1411  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-505

Query Match Score 59.1%; Pred. No. 1e-02; Length 1411;  
Best Local Similarity 76.9%; Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCUGUA 16  
Db 453 AACTCACTCGTGA 465

RESULT 22  
US-09-949-016-4615  
Sequence 4615, Application US/09949016  
GENERAL INFORMATION:  
Patent No. 6812339  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 4615  
LENGTH: 1411  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-4615

Query Match Score 59.1%; Pred. No. 1e-02; Length 1411;  
Best Local Similarity 76.9%; Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCUGUA 16  
Db 453 AACTCACTCGTGA 465

RESULT 23  
US-09-620-312D-452  
Sequence 452, Application US/09620312D  
PATENT NUMBER: 6569652  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Changhua  
APPLICANT: Asundi, Vinod

Query Match Score 59.1%; Pred. No. 1e-02; Length 1411;  
Best Local Similarity 76.9%; Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCUGUA 16  
Db 453 AACTCACTCGTGA 465

RESULT 24  
US-09-221-017B-960/c  
Sequence 960, Application US/09221017B  
PATENT NUMBER: 6444799  
GENERAL INFORMATION:  
APPLICANT: Ross, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastaSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
APPLICATION NUMBER: PP1182

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1546  
FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PP2911  
 FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/AU98/01023  
 FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:  
 NAME: Monroy, Gladys H.  
 REGISTRATION NUMBER: 32,430  
 REFERENCE/DOCKET NUMBER: 27340-20021.00

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-813-5600  
 TELEX: 650-494-0792

INFORMATION FOR SEQ ID NO: 960:  
 SEQUENCES CHARACTERISTICS:  
 LENGTH: 3250 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:  
 ORGANISM: PORYPHYROMONAS GINGIVALIS

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1...3250  
 US-09-221-017B-960

Query Match 59.1%; Score 13; DB 3; Length 3250;  
 Best Local Similarity 76.9%; Pred. No. 97;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUG 13  
 Db 2826 GTGAACTCTACTCG 2814

RESULT 25  
 US-09-060-482-1/C  
 Sequence 1, Application US/09060482  
 GENERAL INFORMATION:  
 PATENT NO. 6468766  
 APPLICANT: Lee, Mu-En  
 APPLICANT: Layne, Matthew D.  
 APPLICANT: Yet, Shaw-Fang  
 TITLE OF INVENTION: AORTIC CARDOXYPEPTIDASE-LIKE POLYPEPTIDE  
 FILE REFERENCE: 0543/036001  
 CURRENT APPLICATION NUMBER: US/09/060,482  
 CURRENT FILING DATE: 1998-04-15  
 EARLIER FILING DATE: 1997-03-14  
 EARLIER APPLICATION NUMBER: US 60\013,439  
 EARLIER FILING DATE: 1996-03-15  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 1  
 LENGTH: 3935  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (140)...(3613)

Query Match 59.1%; Score 13; DB 3; Length 3935;  
 Best Local Similarity 76.9%; Pred. No. 96;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CUCGGAGGCUCTT 22  
 Db 1925 CTCGTGAGCTCT 1913

RESULT 26  
 US-09-949-016-2722/C  
 Sequence 2722, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE REFERENCE: CL0013.07  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 60/241,755  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/237,768  
 PRIOR FILING DATE: 2000-10-03  
 PRIOR APPLICATION NUMBER: 60/231,498  
 PRIOR FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 207012  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 2722  
 LENGTH: 4082  
 TYPE: DNA  
 ORGANISM: Human  
 US-09-949-016-2722

Query Match 59.1%; Score 13; DB 4; Length 4082;  
 Best Local Similarity 76.9%; Pred. No. 96;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CUCGGAGGCUCTT 22  
 Db 2092 CTCCTGAGCTCT 2080

RESULT 27  
 US-09-525-305-50  
 Sequence 50, Application US/09525305  
 Patent No. 6806062  
 GENERAL INFORMATION:  
 APPLICANT: Hjort, Carsten  
 APPLICANT: Hondeel, C.A.M.J.J. van den  
 APPLICANT: Punt, P.J.  
 APPLICANT: Shuren, F.H.J.J.  
 APPLICANT: Christensen, Trove  
 TITLE OF INVENTION: Fungal Transcriptional Activator Useful In Methods For Producing Polypeptides  
 FILE REFERENCE: 5555,400-US  
 CURRENT APPLICATION NUMBER: US/09/525,305  
 CURRENT FILING DATE: 2000-03-14  
 NUMBER OF SEQ ID NOS: 54  
 SEQ ID NO 50  
 LENGTH: 6015  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: pdv8 plasmid  
 US-09-525-305-50

Query Match 59.1%; Score 13; DB 4; Length 6015;  
 Best Local Similarity 76.9%; Pred. No. 95;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 9 ACUGUGAGCUCT 21  
 Db 350 ACTCTGAGCTCT 362

RESULT 28  
 US-09-949-016-12281  
 Sequence 12281, Application US/09949016

```

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 12247
; LENGTH: 6831
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12247

Query Match 59.1%; Score 13; DB 4; Length 14395;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCUGUA 16
Db 11437 AACTCCTCTCTGA 11449

Search completed: July 21, 2005, 00:58:19
Job time : 147 secs

RESULT 29
US-09-949-016-14464/C
; Sequence 14464, Application US/09949016
; Patient No. 6B12339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 14464
; LENGTH: 14205
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14464

Query Match 59.1%; Score 13; DB 4; Length 14205;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CUCUGAGGCUCTT 22
Db 9218 CTGGTAGCTCT 9206

RESULT 30
US-09-949-016-12247
; Sequence 12247, Application US/09949016
; Patient No. 6B12339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:27:36 ; Search time 605 Seconds

(without alignments)

230.700 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaaucacucugaggcuctt 22

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 7173243 seqs, 3172129809 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

## Post-processing: Listing first 300 summaries

Database : Published Applications\_NA \*

```

1: /cgcn2_6_ptodata/2/pubpna/us07_PUBCOMB.seq:*
2: /cgcn2_6_ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgcn2_6_ptodata/2/pubpna/US05__NEW_PUB.seq:*
4: /cgcn2_6_ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgcn2_6_ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgcn2_6_ptodata/2/pubpna/PC07_PUBCOMB.seq:*
7: /cgcn2_6_ptodata/2/pubpna/US08__NEW_PUB.seq:*
8: /cgcn2_6_ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgcn2_6_ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgcn2_6_ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgcn2_6_ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgcn2_6_ptodata/2/pubpna/US09__NEW_PUB.seq:*
13: /cgcn2_6_ptodata/2/pubpna/US09_N_PUBCOMB.seq:*
14: /cgcn2_6_ptodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgcn2_6_ptodata/2/pubpna/US10C__PUBCOMB.seq:*
16: /cgcn2_6_ptodata/2/pubpna/US10_PUBCOMB.seq:*
17: /cgcn2_6_ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgcn2_6_ptodata/2/pubpna/US10F__PUBCOMB.seq:*
19: /cgcn2_6_ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgcn2_6_ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgcn2_6_ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgcn2_6_ptodata/2/pubpna/US11A__NEW_PUB.seq:*
23: /cgcn2_6_ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgcn2_6_ptodata/2/pubpna/US11__NEW_PUB.seq:*
25: /cgcn2_6_ptodata/2/pubpna/US10__NEW_PUB.seq:*
26: /cgcn2_6_ptodata/2/pubpna/US00_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	22	100.0	22	21 US-10-848-737-1	Sequence 1, Appli
2	20	90.9	20	21 US-10-831-901A-780	Sequence 780, Appli
3	20	90.9	525	22 US-10-755-415-166	Sequence 166, Appli
4	20	90.9	1215	21 US-10-699-936-4	Sequence 2966, Appli
5	20	90.9	1706	21 US-10-699-936-14	Sequence 4, Appli
6	20	90.9	1706	21 US-10-889-447-3	Sequence 14, Appli
7	20	90.9	24774	21 US-10-831-901A-29748	Sequence 3, Appli
8	20	90.9	24774	21 US-10-889-447-5	Sequence 5, Appli
9	20	90.9	28920	21 US-10-889-447-6	Sequence 6, Appli
10	20	90.9	28920	21 US-10-831-901A-29740	Sequence 5, Appli
11	20	90.9	28920	21 US-10-889-101-5	Sequence 6, Appli
12	20	90.9	28920	21 US-10-889-101-6	Sequence 5, Appli
13	20	90.9	29013	21 US-10-831-901A-29819	Sequence 29819, A
14	20	90.9	29206	21 US-10-831-901A-29742	Sequence 29742, A
15	20	90.9	29291	21 US-10-831-901A-29738	Sequence 4, Appli
16	20	90.9	29291	21 US-10-889-447-7	Sequence 4, Appli
17	20	90.9	29430	21 US-10-831-901A-29741	Sequence 7, Appli
18	20	90.9	29430	21 US-10-889-447-4	Sequence 4, Appli
19	20	90.9	29430	21 US-10-831-901A-29739	Sequence 4, Appli
20	20	90.9	29430	21 US-10-889-447-3	Sequence 7, Appli
21	20	90.9	29430	21 US-10-831-901A-29758	Sequence 29758, A
22	20	90.9	29430	21 US-10-831-901A-29757	Sequence 29757, A
23	20	90.9	29430	21 US-10-831-901A-29756	Sequence 29756, A
24	20	90.9	29573	21 US-10-831-901A-29802	Sequence 29802, A
25	20	90.9	29573	21 US-10-831-901A-29803	Sequence 29803, A
26	20	90.9	29573	21 US-10-831-901A-29807	Sequence 29807, A
27	20	90.9	29592	21 US-10-831-901A-29820	Sequence 29820, A
28	20	90.9	29705	21 US-10-831-901A-29758	Sequence 29758, A
29	20	90.9	29705	21 US-10-831-901A-29791	Sequence 29791, A
30	20	90.9	29705	21 US-10-831-901A-29756	Sequence 29756, A
31	20	90.9	29706	21 US-10-831-901A-29793	Sequence 29793, A
32	20	90.9	29711	21 US-10-831-901A-29755	Sequence 29755, A
33	20	90.9	29711	21 US-10-831-901A-29757	Sequence 29757, A
34	20	90.9	29711	21 US-10-831-901A-29759	Sequence 29759, A
35	20	90.9	29711	21 US-10-831-901A-29779	Sequence 29779, A
36	20	90.9	29711	21 US-10-831-901A-29790	Sequence 29790, A
37	20	90.9	29711	21 US-10-831-901A-29792	Sequence 29792, A
38	20	90.9	29711	21 US-10-831-901A-29794	Sequence 29794, A
39	20	90.9	29711	21 US-10-831-901A-29815	Sequence 29815, A
40	20	90.9	29715	21 US-10-831-901A-29760	Sequence 29760, A
41	20	90.9	29715	21 US-10-831-901A-29795	Sequence 29795, A
42	20	90.9	29715	21 US-10-831-901A-29794	Sequence 29794, A
43	20	90.9	29720	21 US-10-831-901A-29798	Sequence 29798, A
44	20	90.9	29725	21 US-10-831-901A-29753	Sequence 29753, A
45	20	90.9	29725	21 US-10-831-901A-29774	Sequence 29774, A
46	20	90.9	29725	21 US-10-831-901A-29781	Sequence 29781, A
47	20	90.9	29725	21 US-10-831-901A-29785	Sequence 29785, A
48	20	90.9	29725	21 US-10-831-901A-29715	Sequence 15, Appli
49	20	90.9	29727	21 US-10-827-757-1	Sequence 1, Appli
50	20	90.9	29727	21 US-10-831-901A-29786	Sequence 29816, A
51	20	90.9	29727	21 US-10-831-901A-29798	Sequence 29798, A
52	20	90.9	29727	21 US-10-831-901A-29773	Sequence 29773, A
53	20	90.9	29727	21 US-10-831-901A-29780	Sequence 29780, A
54	20	90.9	29727	21 US-10-831-901A-29782	Sequence 29782, A
55	20	90.9	29727	21 US-10-831-901A-29783	Sequence 29783, A
56	20	90.9	29727	21 US-10-831-901A-29784	Sequence 29784, A
57	20	90.9	29727	21 US-10-831-901A-29812	Sequence 29812, A
58	20	90.9	29727	21 US-10-831-901A-29813	Sequence 29813, A
59	20	90.9	29727	21 US-10-831-901A-29823	Sequence 29823, A
60	20	90.9	29729	21 US-10-831-901A-29822	Sequence 29822, A
61	20	90.9	29729	21 US-10-831-901A-29825	Sequence 29825, A
62	20	90.9	29729	21 US-10-831-901A-29826	Sequence 29826, A
63	20	90.9	29729	21 US-10-831-901A-29827	Sequence 29827, A
64	20	90.9	29729	21 US-10-831-901A-29821	Sequence 29821, A
65	20	90.9	29729	21 US-10-831-901A-29823	Sequence 29823, A
66	20	90.9	29729	21 US-10-831-901A-29824	Sequence 29824, A
67	20	90.9	29729	21 US-10-831-901A-29825	Sequence 29825, A
68	20	90.9	29729	21 US-10-831-901A-29827	Sequence 29827, A
69	20	90.9	29729	21 US-10-831-901A-29828	Sequence 29828, A
70	20	90.9	29729	21 US-10-831-901A-29829	Sequence 29829, A
71	20	90.9	29729	21 US-10-831-901A-29830	Sequence 29830, A
72	20	90.9	29729	21 US-10-831-901A-29831	Sequence 29831, A
73	20	90.9	29731	21 US-10-831-901A-29797	Sequence 29797, A
74	20	90.9	29732	21 US-10-831-901A-29771	Sequence 29771, A
75	20	90.9	29732	21 US-10-831-901A-29788	Sequence 29788, A
76	20	90.9	29735	21 US-10-831-901A-29814	Sequence 29814, A
77	20	90.9	29736	21 US-10-833-729-17	Sequence 17, Appli
78	20	90.9	29736	21 US-10-833-729-17	Sequence 9, Appli
79	20	90.9	29736	21 US-10-699-936-3	Sequence 3, Appli
80	20	90.9	29736	21 US-10-831-901A-16	Sequence 16, Appli

81 20 90.9 29736 21 US-10-831-901A-29746 Sequence 29746, A  
 82 20 90.9 29736 21 US-10-831-901A-29747 Sequence 29747, A  
 83 20 90.9 29736 21 US-10-831-901A-29749 Sequence 29749, A  
 84 20 90.9 29736 21 US-10-831-901A-29750 Sequence 29750, A  
 85 20 90.9 29736 21 US-10-831-901A-29763 Sequence 29763, A  
 86 20 90.9 29736 21 US-10-831-901A-29789 Sequence 29789, A  
 87 20 90.9 29736 21 US-10-831-901A-29804 Sequence 29804, A  
 88 20 90.9 29736 21 US-10-831-901A-29815 Sequence 29805, A  
 89 20 90.9 29736 21 US-10-831-901A-29816 Sequence 29806, A  
 90 20 90.9 29736 21 US-10-888-101-9 Sequence 9, App1  
 91 20 90.9 29736 21 US-10-831-901A-29813 Sequence 29808, A  
 92 20 90.9 29738 21 US-10-831-901A-29816 Sequence 29810, A  
 93 20 90.9 29738 21 US-10-831-901A-29810 Sequence 29811, A  
 94 20 90.9 29740 21 US-10-831-901A-29770 Sequence 29770, A  
 95 20 90.9 29740 21 US-10-831-901A-29787 Sequence 29787, A  
 96 20 90.9 29740 21 US-10-831-901A-29799 Sequence 29799, A  
 97 20 90.9 29740 21 US-10-831-901A-29818 Sequence 29818, A  
 98 20 90.9 29741 21 US-10-831-901A-29796 Sequence 29796, A  
 99 20 90.9 29741 21 US-10-831-901A-29817 Sequence 29817, A  
 100 20 90.9 29742 21 US-10-831-729-16 Sequence 16, App1  
 101 20 90.9 29742 21 US-10-808-187-15 Sequence 15, App1  
 102 20 90.9 29742 21 US-10-808-187-16 Sequence 16, App1  
 103 20 90.9 29742 21 US-10-808-187-240 Sequence 240, App1  
 C 105 20 90.9 29742 21 US-10-808-187-737 Sequence 737, App1  
 C 106 20 90.9 29742 21 US-10-808-187-1108 Sequence 1108, App1  
 C 107 20 90.9 29742 21 US-10-808-187-1590 Sequence 1965, App1  
 108 20 90.9 29742 21 US-10-888-447-10 Sequence 10, App1  
 109 20 90.9 29742 21 US-10-831-901A-29744 Sequence 29744, A  
 110 20 90.9 29742 21 US-10-888-101-10 Sequence 10, App1  
 111 20 90.9 29742 22 US-10-843-527-238914 Sequence 238194, App1  
 112 20 90.9 29742 21 US-10-808-187-1965 Sequence 29768, A  
 113 20 90.9 29745 21 US-10-831-901A-29811 Sequence 29811, A  
 114 20 90.9 29749 21 US-10-831-901A-29809 Sequence 29809, A  
 115 20 90.9 29751 21 US-10-855-529-1 Sequence 14, App1  
 116 20 90.9 29751 21 US-10-831-901A-29751 Sequence 1, App1  
 117 20 90.9 29751 21 US-10-626-879-67 Sequence 67, App1  
 118 20 90.9 29751 21 US-10-888-447-1 Sequence 1, App1  
 119 20 90.9 29751 21 US-10-888-447-2 Sequence 2, App1  
 120 20 90.9 29751 21 US-10-699-936-2 Sequence 2, App1  
 121 20 90.9 29751 21 US-10-831-901A-29751 Sequence 29751, A  
 122 20 90.9 29751 21 US-10-831-901A-29752 Sequence 29752, A  
 123 20 90.9 29751 21 US-10-831-901A-29778 Sequence 29778, A  
 124 20 90.9 29751 21 US-10-831-901A-29801 Sequence 29801, A  
 125 20 90.9 29751 21 US-10-888-101-1 Sequence 1, App1  
 126 20 90.9 29751 21 US-10-888-101-2 Sequence 2, App1  
 127 20 90.9 29751 22 US-10-831-901A-29815 Sequence 29815, A  
 128 20 90.9 29754 21 US-10-831-901A-29800 Sequence 29800, A  
 129 20 90.9 29757 21 US-10-831-901A-29769 Sequence 29769, A  
 130 20 90.9 29757 21 US-10-831-901A-29786 Sequence 29786, A  
 131 20 90.9 29760 21 US-10-888-401-1 Sequence 1, App1  
 C 132 19 86.4 20 21 US-10-831-901A-779 Sequence 779, App1  
 C 133 19 86.4 20 21 US-10-831-901A-781 Sequence 781, App1  
 C 134 19 81.8 20 21 US-10-831-901A-778 Sequence 778, App1  
 C 135 18 81.8 20 21 US-10-831-901A-782 Sequence 782, App1  
 C 136 17 77.3 20 21 US-10-831-901A-777 Sequence 777, App1  
 C 137 17 77.3 20 21 US-10-831-901A-783 Sequence 783, App1  
 C 138 16 72.7 20 21 US-10-831-901A-776 Sequence 776, App1  
 C 139 16 72.7 20 21 US-10-831-901A-776 Sequence 776, App1  
 C 140 16 72.7 20 21 US-10-487-901-5047 Sequence 5047, App1  
 C 141 16 72.7 20 21 US-10-487-901-5767 Sequence 5767, App1  
 C 142 16 72.7 20 21 US-10-487-901-1715 Sequence 1715, App1  
 C 143 16 72.7 20 21 US-10-487-901-5029 Sequence 5029, App1  
 C 144 16 72.7 20 21 US-10-437-963-10106 Sequence 101306, App1  
 C 145 15 68.2 20 21 US-10-831-901A-775 Sequence 775, App1  
 C 146 15 68.2 20 21 US-10-831-901A-785 Sequence 785, App1  
 C 147 15 68.2 25 22 US-10-719-956-515621 Sequence 515621, A  
 C 148 15 68.2 25 22 US-10-719-956-512656 Sequence 512656, A  
 C 149 15 68.2 537 17 US-10-28-122A-38146 Sequence 38146, A  
 C 150 15 68.2 627 14 US-10-00-256A-81 Sequence 81, App1  
 C 151 15 68.2 820 19 US-10-767-795-2281 Sequence 2281, App1  
 C 152 15 68.2 1101 19 US-10-767-701-619 Sequence 619, App1  
 C 153 15 68.2 1820 9 US-09-864-761-19662 Sequence 19662, A

15 68.2 1870 9 US-09-864-761-21483 Sequence 21483, A  
 15 68.2 1966 9 US-09-864-788-2881 Sequence 2881, App  
 15 68.2 4317 19 US-10-75-889-778 Sequence 778, App  
 C 154 15 68.2 5242 18 US-10-620-914-43 Sequence 43, App1  
 C 155 15 68.2 5242 18 US-10-620-914-43 Sequence 74, App  
 C 156 15 68.2 5242 18 US-10-620-914-43 Sequence 74, App  
 C 157 15 68.2 5242 18 US-10-620-914-43 Sequence 43, App1  
 C 158 14 63.6 20 21 US-10-831-901A-774 Sequence 774, App  
 C 159 14 63.6 20 21 US-10-831-901A-786 Sequence 786, App  
 C 160 14 63.6 22 22 US-10-724-972A-609 Sequence 609, App  
 C 161 14 63.6 348 22 US-10-724-972A-609 Sequence 609, App  
 C 162 14 63.6 535 13 US-10-027-632-18722 Sequence 187522, A  
 C 163 14 63.6 535 17 US-10-027-632-18722 Sequence 187522, A  
 C 164 14 63.6 603 20 21 US-10-445-115-132098 Sequence 132098, A  
 C 165 14 63.6 744 19 US-10-767-701-7756 Sequence 7756, App  
 C 166 14 63.6 932 13 US-10-027-632-170009 Sequence 170009, A  
 C 167 14 63.6 1278 17 US-10-027-632-170009 Sequence 170009, A  
 C 168 14 63.6 932 13 US-10-027-632-170010 Sequence 170010, A  
 C 169 14 63.6 932 17 US-10-027-632-170010 Sequence 170010, A  
 C 170 14 63.6 932 17 US-10-027-632-170011 Sequence 170011, A  
 C 171 14 63.6 932 17 US-10-027-632-170011 Sequence 170011, A  
 C 172 14 63.6 1278 17 US-10-027-632-170011 Sequence 170011, A  
 C 173 14 63.6 932 17 US-10-027-632-170011 Sequence 170011, A  
 C 174 14 63.6 2950 19 US-10-330-797-156 Sequence 156, App  
 C 175 14 63.6 3504 19 US-10-330-797-156 Sequence 156, App  
 C 176 14 63.6 3705 19 US-10-337-963-21697 Sequence 21697, A  
 C 177 14 63.6 4314 17 US-10-282-192-345758 Sequence 345758, A  
 C 178 14 63.6 4704 19 US-10-337-963-21704 Sequence 21704, A  
 C 179 14 63.6 4889 19 US-10-337-963-40278 Sequence 40278, A  
 C 180 14 63.6 5004 19 US-10-437-963-40272 Sequence 40272, A  
 C 181 14 63.6 5388 19 US-10-337-963-40273 Sequence 40273, A  
 C 182 14 63.6 8937 19 US-10-437-963-40275 Sequence 40275, A  
 C 183 14 63.6 47493 18 US-10-052-482-50215 Sequence 50215, A  
 C 184 14 63.6 76180 19 US-10-032-281-492 Sequence 492, App  
 C 185 14 63.6 76698 21 US-10-936-730-310 Sequence 30, App  
 C 186 14 63.6 76698 22 US-10-948-947A-1 Sequence 1, App1  
 C 187 14 63.6 110838 22 US-10-040-512-41 Sequence 41, App1  
 C 188 14 63.6 247544 19 US-10-322-696-55 Sequence 55, App1  
 C 189 13 59.1 20 21 US-10-831-901A-773 Sequence 773, App  
 C 190 13 59.1 20 21 US-10-831-901A-787 Sequence 787, App  
 C 191 13 59.1 21 21 US-10-842-758-110 Sequence 110, App  
 C 192 13 59.1 21 21 US-10-174-333-110 Sequence 110, App  
 C 193 13 59.1 21 21 US-10-174-333-110 Sequence 110, App  
 C 194 13 59.1 22 22 US-10-315-977-9995 Sequence 9995, App  
 C 195 13 59.1 22 22 US-10-719-956-73668 Sequence 73668, A  
 C 196 13 59.1 25 22 US-10-719-956-78611 Sequence 78611, A  
 C 197 13 59.1 25 22 US-10-719-956-30986 Sequence 308817, A  
 C 198 13 59.1 25 22 US-10-719-956-31234 Sequence 312434, A  
 C 199 13 59.1 25 22 US-10-719-956-501537 Sequence 501537, A  
 C 200 13 59.1 200 16 Sequence 22454, A  
 C 201 13 59.1 275 20 Sequence 16480, A  
 C 202 13 59.1 304 21 Sequence 97, App1  
 C 203 13 59.1 305 9 Sequence 2109, Ap  
 C 204 13 59.1 314 20 US-10-125-115-33053 Sequence 33053, A  
 C 205 13 59.1 329 22 US-10-425-115-72056 Sequence 72056, A  
 C 206 13 59.1 382 20 Sequence 145414, A  
 C 207 13 59.1 399 18 US-10-425-115-2454 Sequence 2454, A  
 C 208 13 59.1 409 18 US-10-425-115-16480 Sequence 16480, A  
 C 209 13 59.1 435 17 US-10-425-115-16881 Sequence 16881, A  
 C 210 13 59.1 445 14 US-10-060-036-3310 Sequence 3310, Ap  
 C 211 13 59.1 420 17 US-10-242-53A-4252 Sequence 4252, Ap  
 C 212 13 59.1 420 17 US-10-918-995-7072 Sequence 7072, Ap  
 C 213 13 59.1 420 18 US-10-425-115-145414 Sequence 145414, A  
 C 214 13 59.1 435 17 US-10-425-115-27144 Sequence 271544, A  
 C 215 13 59.1 445 14 US-10-060-036-3310 Sequence 3310, Ap  
 C 216 13 59.1 413 11 US-10-09-32A-627A-4252 Sequence 4252, Ap  
 C 217 13 59.1 486 10 Sequence 55663, A  
 C 218 13 59.1 420 18 US-10-085-783A-55663 Sequence 55663, A  
 C 219 13 59.1 420 18 Sequence 55663, A  
 C 220 13 59.1 435 17 US-10-057-632-212656 Sequence 212656, A  
 C 221 13 59.1 520 13 Sequence 315678, A  
 C 222 13 59.1 520 17 US-10-027-632-212656 Sequence 212656, A  
 C 223 13 59.1 545 13 Sequence 65663, A  
 C 224 13 59.1 545 13 Sequence 65663, A  
 C 225 13 59.1 545 13 Sequence 65663, A  
 C 226 13 59.1 545 13 Sequence 65663, A

Sequence 7568, Ap												
227	13	59.1	17	US-10-027-632-6883	Sequence 6883, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
228	13	59.1	17	US-10-027-632-6884	Sequence 6884, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
229	13	59.1	17	US-10-027-632-6885	Sequence 6885, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
230	13	59.1	17	US-10-027-632-147918	Sequence 147918,	300	13	59.1	1767	15	US-10-128-714-7568	
231	13	59.1	17	US-10-027-632-147918	Sequence 147918,	300	13	59.1	1767	15	US-10-128-714-7568	
232	13	59.1	17	US-09-038-842A-1538	Sequence 1538, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
233	13	59.1	17	US-09-038-842A-1538	Sequence 1538, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
234	13	59.1	17	US-10-487-301-7387	Sequence 7387, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
235	13	59.1	17	US-10-027-632-280740	Sequence 280740,	300	13	59.1	1767	15	US-10-128-714-7568	
236	13	59.1	17	US-10-027-632-280741	Sequence 280741,	300	13	59.1	1767	15	US-10-128-714-7568	
237	13	59.1	17	US-10-027-632-280740	Sequence 280740,	300	13	59.1	1767	15	US-10-128-714-7568	
238	13	59.1	17	US-10-027-632-280741	Sequence 280741,	300	13	59.1	1767	15	US-10-128-714-7568	
239	13	59.1	17	US-10-027-632-32224	Sequence 32224, A	300	13	59.1	1767	15	US-10-128-714-7568	
240	13	59.1	17	US-10-027-632-32224	Sequence 32224, A	300	13	59.1	1767	15	US-10-128-714-7568	
241	13	59.1	17	US-10-027-632-32224	Sequence 32224, A	300	13	59.1	1767	15	US-10-128-714-7568	
242	13	59.1	17	US-10-027-632-32224	Sequence 32224, A	300	13	59.1	1767	15	US-10-128-714-7568	
243	13	59.1	17	US-10-425-114-25674	Sequence 4457, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
244	13	59.1	17	US-09-815-242-6948	Sequence 6948, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
245	13	59.1	17	US-10-282-122A-22024	Sequence 22024, A	300	13	59.1	1767	15	US-10-128-714-7568	
246	13	59.1	17	US-10-487-301-3701	Sequence 3701, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
247	13	59.1	17	US-10-425-115-141170	Sequence 141170,	300	13	59.1	1767	15	US-10-128-714-7568	
248	13	59.1	17	US-09-770-445-832	Sequence 832, App	300	13	59.1	1767	15	US-10-128-714-7568	
249	13	59.1	17	US-10-437-663-47033	Sequence 47033, A	300	13	59.1	1767	15	US-10-128-714-7568	
250	13	59.1	17	US-10-425-115-11740	Sequence 11740, A	300	13	59.1	1767	15	US-10-128-714-7568	
251	13	59.1	17	US-10-425-115-11740	Sequence 11740, A	300	13	59.1	1767	15	US-10-128-714-7568	
252	13	59.1	17	US-09-815-242-7527	Sequence 7527, Ap	300	13	59.1	1767	15	US-10-128-714-7568	
253	13	59.1	17	US-10-282-122A-22850	Sequence 22850, A	300	13	59.1	1767	15	US-10-128-714-7568	
254	13	59.1	17	US-10-335-977-120	Sequence 120, App	300	13	59.1	1767	15	US-10-128-714-7568	
255	13	59.1	17	US-10-335-977-121	Sequence 121, App	300	13	59.1	1767	15	US-10-128-714-7568	
256	13	59.1	17	US-10-425-115-11741	Sequence 11741, A	300	13	59.1	1767	15	US-10-128-714-7568	
257	13	59.1	17	US-10-279-579A-3	Sequence 3, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
258	13	59.1	17	US-10-335-977-122	Sequence 122, App	300	13	59.1	1767	15	US-10-128-714-7568	
259	13	59.1	17	US-10-357-930-3029	Sequence 3029, A	300	13	59.1	1767	15	US-10-128-714-7568	
260	13	59.1	17	US-10-425-115-12436	Sequence 12436, A	300	13	59.1	1767	15	US-10-128-714-7568	
261	13	59.1	17	US-09-925-301-14	Sequence 14, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
262	13	59.1	17	US-10-425-115-134955	Sequence 134955, A	300	13	59.1	1767	15	US-10-128-714-7568	
263	13	59.1	17	US-10-027-632-120838	Sequence 120838, A	300	13	59.1	1767	15	US-10-128-714-7568	
264	13	59.1	17	US-10-027-632-120839	Sequence 120839,	300	13	59.1	1767	15	US-10-128-714-7568	
265	13	59.1	17	US-10-027-632-120840	Sequence 120840,	300	13	59.1	1767	15	US-10-128-714-7568	
266	13	59.1	17	US-10-027-632-120838	Sequence 120838,	300	13	59.1	1767	15	US-10-128-714-7568	
267	13	59.1	17	US-10-027-632-120839	Sequence 120839,	300	13	59.1	1767	15	US-10-128-714-7568	
268	13	59.1	17	US-10-027-632-120840	Sequence 120840,	300	13	59.1	1767	15	US-10-128-714-7568	
269	13	59.1	17	US-10-027-632-120841	Sequence 120841, App	300	13	59.1	1767	15	US-10-128-714-7568	
270	13	59.1	17	US-10-286-264-33	Sequence 33, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
271	13	59.1	17	US-10-374-780A-127	Sequence 127, App	300	13	59.1	1767	15	US-10-128-714-7568	
272	13	59.1	17	US-10-374-780A-13	Sequence 13, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
273	13	59.1	17	US-10-412-699B-67	Sequence 67, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
274	13	59.1	17	US-09-738-626-532	Sequence 532, App	300	13	59.1	1767	15	US-10-128-714-7568	
275	13	59.1	17	US-10-767-01-13098	Sequence 13098, A	300	13	59.1	1767	15	US-10-128-714-7568	
276	13	59.1	17	US-10-369-193-22586	Sequence 22586, A	300	13	59.1	1767	15	US-10-128-714-7568	
277	13	59.1	17	US-10-382-122A-22465	Sequence 22465, A	300	13	59.1	1767	15	US-10-128-714-7568	
278	13	59.1	17	US-10-425-114-281069	Sequence 281069, A	300	13	59.1	1767	15	US-10-128-714-7568	
279	13	59.1	17	US-10-225-066A-657	Sequence 657, App	300	13	59.1	1767	15	US-10-128-714-7568	
280	13	59.1	17	US-10-764-881-47	Sequence 47, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
281	13	59.1	17	US-09-764-881-47	Sequence 47, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
282	13	59.1	17	US-10-425-114-28742	Sequence 28742, A	300	13	59.1	1767	15	US-10-128-714-7568	
283	13	59.1	17	US-10-425-115-11737	Sequence 11737, A	300	13	59.1	1767	15	US-10-128-714-7568	
284	13	59.1	17	US-10-424-599-45112	Sequence 45112, A	300	13	59.1	1767	15	US-10-128-714-7568	
285	13	59.1	17	US-10-037-270-452	Sequence 452, App	300	13	59.1	1767	15	US-10-128-714-7568	
286	13	59.1	17	US-10-117-72-452	Sequence 452, App	300	13	59.1	1767	15	US-10-128-714-7568	
287	13	59.1	17	US-09-764-881-47	Sequence 47, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
288	13	59.1	17	US-09-764-881-47	Sequence 47, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
289	13	59.1	17	US-09-764-881-47	Sequence 47, Appli	300	13	59.1	1767	15	US-10-128-714-7568	
290	13	59.1	17	US-10-242-115-49236	Sequence 49236, A	300	13	59.1	1767	15	US-10-128-714-7568	
291	13	59.1	17	US-10-158-057-154	Sequence 154, App	300	13	59.1	1767	15	US-10-128-714-7568	
292	13	59.1	17	US-10-930-4802	Sequence 4802, App	300	13	59.1	1767	15	US-10-128-714-7568	
293	13	59.1	17	US-10-425-114-5598	Sequence 5598, App	300	13	59.1	1767	15	US-10-128-714-7568	
294	13	59.1	17	US-10-425-115-49236	Sequence 49236, A	300	13	59.1	1767	15	US-10-128-714-7568	
295	13	59.1	17	US-10-425-115-116401	Sequence 116401, App	300	13	59.1	1767	15	US-10-128-714-7568	
296	13	59.1	17	US-10-425-114-35588	Sequence 35588, A	300	13	59.1	1767	15	US-10-128-714-7568	
297	13	59.1	17	US-10-374-780A-972	Sequence 972, App	300	13	59.1	1767	15	US-10-128-714-7568	
298	13	59.1	17	US-10-425-114-957	Sequence 957, App	300	13	59.1	1767	15	US-10-128-714-7568	
299	13	59.1	17	US-10-467-779	Sequence 779, App	300	13	59.1	1767	15	US-10-128-714-7568	

```

; PRIORITY APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIORITY APPLICATION NUMBER: 60/477,637
; PRIORITY APPLICATION NUMBER: US/10/831,901A
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIORITY APPLICATION NUMBER: 60/466,426
; PRIORITY FILING DATE: 2003-04-28
; PRIORITY APPLICATION NUMBER: 60/468,562
; PRIORITY FILING DATE: 2003-05-06
; PRIORITY APPLICATION NUMBER: 60/467,770
; PRIORITY FILING DATE: 2003-04-30
; PRIORITY APPLICATION NUMBER: 60/468,627
; PRIORITY FILING DATE: 2003-05-06
; PRIORITY APPLICATION NUMBER: 60/477,637
; PRIORITY FILING DATE: 2003-06-10
; PRIORITY APPLICATION NUMBER: 60/483,579
; PRIORITY FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 780
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-780

Qy      1 GUGAACUCACUCUGAGCUC 20
Db      20 GTGAACTACTCGTAGCTC 1

RESULT 3
US-10-755-415-166
Sequence 166, Application US/10755415
Publication No. US2005013480A1
GENERAL INFORMATION:
; APPLICANT: BRAHMACHARI, SAMIR KUMAR
; APPLICANT: DASH, DEBASIS
; APPLICANT: SHARMA, RAMAKANT
; APPLICANT: MAHESHWARI, JITENDRA KUMAR
TITLE OF INVENTION: A COMPUTER BASED VERSATILE METHOD FOR IDENTIFYING PROTEIN CODING
FILE REFERENCE: 02633-00029
CURRENT FILING DATE: 2004-01-13
PRIORITY APPLICATION NUMBER: 10/727,989
PRIOR FILING DATE: 2003-12-05
NUMBER OF SEQ ID NOS: 373
SOFTWARE: Patentin version 3.3
SEQ ID NO 166
LENGTH: 925
; TYPE: DNA
; ORGANISM: Sars coronavirus
US-10-755-415-166

Query Match      90.9%; Score 20; DB 22; Length 525;
Best Local Similarity 75.0%; Pred. No. 0.014;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GUGAACUCACUCUGAGCUC 20
Db      76 GTGAACTACTCGTAGCTC 95

```

```

RESULT 4
US-10-831-901A-29766
Sequence 29766, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hoststader, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Taylor, Jill

Qy      1 GUGAACUCACUCUGAGCUC 20
Db      76 GTGAACTACTCGTAGCTC 95

```

```

RESULT 5
US-10-699-936-4
Sequence 4, Application US/10699936
Publication No. US2005009582A1
GENERAL INFORMATION:
; APPLICANT: Gilliam-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollieck, Joseph D.
; APPLICANT: Title of Invention: Compositions and Methods for Detecting Severe Acute Respiratory
; Syndrome Coronavirus
; FILE REFERENCE: DHL-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 1706
; TYPE: DNA
; ORGANISM: SARS-CoV Shanghai LY
US-10-699-936-4

Query Match      90.9%; Score 20; DB 21; Length 1706;
Best Local Similarity 75.0%; Pred. No. 0.012;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GUGAACUCACUCUGAGCUC 20
Db      697 GTGAACTACTCGTAGCTC 716

```

```

RESULT 6
US-10-699-936-14
Sequence 14, Application US/10699936
Publication No. US2005009582A1
GENERAL INFORMATION:
; APPLICANT: Gilliam-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Wentworth, David E.
; APPLICANT: Scholl, David R.
; APPLICANT: Jollieck, Joseph D.
; APPLICANT: Title of Invention: Compositions and Methods for Detecting Severe Acute Respiratory
; Syndrome Coronavirus
; FILE REFERENCE: DHL-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 1706
; TYPE: DNA
; ORGANISM: SARS-CoV Shanghai LY
US-10-699-936-14

Query Match      90.9%; Score 20; DB 21; Length 1706;
Best Local Similarity 75.0%; Pred. No. 0.012;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GUGAACUCACUCUGAGCUC 20
Db      697 GTGAACTACTCGTAGCTC 716

```

```

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS083-100 (BIO00080US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIORITY APPLICATION NUMBER: 60/466,426
; PRIORITY FILING DATE: 2003-04-28
; PRIORITY APPLICATION NUMBER: 60/468,562
; PRIORITY FILING DATE: 2003-05-06
; PRIORITY APPLICATION NUMBER: 60/467,770
; PRIORITY FILING DATE: 2003-04-30
; PRIORITY APPLICATION NUMBER: 60/468,627
; PRIORITY FILING DATE: 2003-05-06
; PRIORITY APPLICATION NUMBER: 60/477,637
; PRIORITY FILING DATE: 2003-06-10
; PRIORITY APPLICATION NUMBER: 60/483,579
; PRIORITY FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 780
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-29766

Qy      1 GUGAACUCACUCUGAGCUC 20
Db      20 GTGAACTACTCGTAGCTC 1

Query Match      90.9%; Score 20; DB 21; Length 1215;
Best Local Similarity 75.0%; Pred. No. 0.013;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
; ORGANISM: SARS Coronavirus
US-10-831-901A-29766

RESULT 5
US-10-699-936-4
Sequence 4, Application US/10699936
Publication No. US2005009582A1
GENERAL INFORMATION:
; APPLICANT: Gilliam-Ross, Laura
; APPLICANT: Taylor, Jill
; APPLICANT: Scholl, David R.
; APPLICANT: Wentworth, David E.
; APPLICANT: Jollieck, Joseph D.
; APPLICANT: Title of Invention: Compositions and Methods for Detecting Severe Acute Respiratory
; Syndrome Coronavirus
; FILE REFERENCE: DHL-07986
; CURRENT APPLICATION NUMBER: US/10/699,936
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 1706
; TYPE: DNA
; ORGANISM: SARS-CoV Shanghai LY
US-10-699-936-4

Query Match      90.9%; Score 20; DB 21; Length 1706;
Best Local Similarity 75.0%; Pred. No. 0.012;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GUGAACUCACUCUGAGCUC 20
Db      697 GTGAACTACTCGTAGCTC 716

```

APPLICANT: Scholl, David R.  
 APPLICANT: Wentworth, David E.  
 APPLICANT: Jollie, Joseph D.  
 TITLE OF INVENTION: Compositions And Methods For Detecting Severe Acute Respiratory Syndrome Coronavirus  
 FILE REFERENCE: DHI-07986  
 CURRENT APPLICATION NUMBER: US/10/699,936  
 CURRENT FILING DATE: 2003-11-03  
 NUMBER OF SEQ ID NOS: 97  
 SEQ ID NO 14  
 LENGTH: 1706  
 TYPE: DNA  
 ORGANISM: SARS coronavirus Shanghai LY  
 US-10-699-936-14

Query Match 90.9%; Score 20; DB 21; Length 1706;  
 Best Local Similarity 75.0%; Pred. No. 0.012; Mismatches 5; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Number of SEQ ID NOS: 30063

Qy 1 GUGAACUCACUGGAGGCU 20  
 Db 697 GTGAATCTACTCGTGTGCTC 716

---

RESULT 7  
 US-10-889-447-3  
 Sequence 3, Application US/10889447  
 Publication No. US20050075307A1  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, C. Frank  
 NUMBER OF SEQ ID NOS: 241  
 FILE REFERENCE: RTS-0685US  
 CURRENT APPLICATION NUMBER: US/10/889,447  
 CURRENT FILING DATE: 2004-07-12  
 PRIOR APPLICATION NUMBER: 60/486,670  
 PRIOR FILING DATE: 2003-07-12  
 NUMBER OF SEQ ID NOS: 241  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 3  
 LENGTH: 24774  
 TYPE: DNA  
 ORGANISM: SARS coronavirus isolate BJ01

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION:

OTHER INFORMATION: n is any nucleotide  
 US-10-889-447-3

Query Match 90.9%; Score 20; DB 21; Length 24774;  
 Best Local Similarity 75.0%; Pred. No. 0.009; Mismatches 5; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Number of SEQ ID NOS: 298

Qy 1 GUGAACUCACUGGAGGCU 20  
 Db 706 GTGAATCTACTCGTGTGCTC 725

---

RESULT 8  
 US-10-831-901A-29748  
 Sequence 29748, Application US/10831901A  
 Publication No. US2005100885A1  
 GENERAL INFORMATION:  
 APPLICANT: Cooke, Stanley T.  
 APPLICANT: Eckert, David J.  
 APPLICANT: Sampath, Rangarajan  
 APPLICANT: Freier, Susan M.  
 APPLICANT: Massire, Christian  
 APPLICANT: Hofstader, Steven A.  
 APPLICANT: Lowery, Kristin Sannes  
 APPLICANT: Swayne, Eric  
 APPLICANT: Baker, Brenda F.

APPLICANT: Bennett, C. Frank  
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)  
 FILE REFERENCE: ISIS0083-100 (BIOL008US)  
 CURRENT APPLICATION NUMBER: US/10/831,901A  
 CURRENT FILING DATE: 2004-04-26  
 PRIOR APPLICATION NUMBER: 60/466,426  
 PRIOR APPLICATION NUMBER: 60/468,562  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR APPLICATION NUMBER: 60/467,770  
 PRIOR APPLICATION NUMBER: 60/468,627  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR APPLICATION NUMBER: 60/483,579  
 PRIOR APPLICATION NUMBER: 60/486,27  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 29748  
 LENGTH: 24774  
 TYPE: DNA  
 ORGANISM: SARS Coronavirus  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 960-959, 2089-2188, 2478-2577, 2877-2976, 3576-3675, 3865-3964,  
 ; LOCATION: 4134-4233, 5781-5811, 5783-5837, 7438-7537, 7837-7936,  
 ; LOCATION: 8616-8715, 12025-12124, 13984-14003, 16463-16562, 16922-17031,  
 ; LOCATION: 1738-17480, 18090-18189, 19019-19118, 19478-19577, 20357-20456,  
 ; LOCATION: 21088-21185, 21945-22044, 23174-23273, 23531  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-10-831-901A-29748

Query Match 90.9%; Score 20; DB 21; Length 24774;  
 Best Local Similarity 75.0%; Pred. No. 0.009; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GUGACUCACUGGAGGCU 20  
 Db 706 GTGAATCTACTCGTGTGCTC 725

---

RESULT 9  
 US-10-889-101-3  
 Sequence 3, Application US/10889101  
 Publication No. US20050107324A1  
 GENERAL INFORMATION:  
 APPLICANT: Dobie, Kenneth W.  
 APPLICANT: Jain, Ravi  
 APPLICANT: Doble, Kenneth W.  
 APPLICANT: Jain, Ravi  
 FILE REFERENCE: ISIS0101-100 (RTS-0655US)  
 CURRENT APPLICATION NUMBER: US/10/889,101  
 CURRENT FILING DATE: 2004-07-12  
 PRIOR APPLICATION NUMBER: 60/486,652  
 PRIOR FILING DATE: 2003-07-12  
 NUMBER OF SEQ ID NOS: 298  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 3  
 LENGTH: 24774  
 TYPE: DNA  
 ORGANISM: SARS Coronavirus isolate BJ01

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION:

OTHER INFORMATION: n is any nucleotide  
 US-10-889-101-3

Query Match 90.9%; Score 20; DB 21; Length 24774;  
 Best Local Similarity 75.0%; Pred. No. 0.009; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGGAGGCU 20  
 Db 706 GTGAATCTACTCGTGTGCTC 725

---

Query Match 90.9%; Score 20; DB 21; Length 24774;  
 Best Local Similarity 75.0%; Pred. No. 0.009; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCCUGAGCUC 20  
 Db 706 GTGAACTCTCGAGCTC 725

RESULT 10  
 US-10-889-447-5  
 ; Sequence 5, Application US/10889447  
 ; Publication No. US20050073307A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, C. Frank  
 ; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION  
 ; FILE REFERENCE: RTS-068505  
 ; CURRENT APPLICATION NUMBER: US/10/889,447  
 ; CURRENT FILING DATE: 2004-07-12  
 ; PRIOR APPLICATION NUMBER: 60/486,670  
 ; PRIOR FILING DATE: 2003-07-12  
 ; NUMBER OF SEQ ID NOS: 241  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 5  
 ; LENGTH: 28920  
 ; TYPE: DNA  
 ; ORGANISM: SARS coronavirus isolate BJ03  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION:  
 ; OTHER INFORMATION: n is any nucleotide  
 US-10-889-447-5

Query Match 90.9%; Score 20; DB 21; Length 28920;  
 Best Local Similarity 75.0%; Pred. No. 0.0089;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCCUGAGCUC 20  
 Db 776 GTGAACTCTACTCGTGAAGCTC 795

RESULT 11  
 US-10-889-447-6  
 ; Sequence 6, Application US/10889447  
 ; Publication No. US20050073307A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, C. Frank  
 ; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION  
 ; FILE REFERENCE: RTS-068505  
 ; CURRENT APPLICATION NUMBER: US/10/889,447  
 ; CURRENT FILING DATE: 2004-07-12  
 ; PRIOR APPLICATION NUMBER: 60/486,670  
 ; PRIOR FILING DATE: 2003-07-12  
 ; NUMBER OF SEQ ID NOS: 241  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 6  
 ; LENGTH: 28920  
 ; TYPE: DNA  
 ; ORGANISM: SARS coronavirus isolate BJ04  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION:  
 ; OTHER INFORMATION: n is any nucleotide  
 US-10-889-447-6

Query Match 90.9%; Score 20; DB 21; Length 28920;  
 Best Local Similarity 75.0%; Pred. No. 0.0089;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCCUGAGCUC 20  
 Db 776 GTGAACTCTACTCGTGAAGCTC 795

RESULT 12  
 US-10-831-901A-29740  
 ; Sequence 29740, Application US/10831901A  
 ; Publication No. US2005010085A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cooke, Stanley T.  
 ; APPLICANT: Ecker, David J.  
 ; APPLICANT: Sampath, Rangarajan  
 ; APPLICANT: Freier, Susan M.  
 ; APPLICANT: Massire, Christian A.  
 ; APPLICANT: Holstader, Steven A.  
 ; APPLICANT: Lowery, Kristin Sannes  
 ; APPLICANT: Swayze, Eric  
 ; APPLICANT: Baker, Brenda F.  
 ; APPLICANT: Bennett, C. Frank  
 ; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)  
 ; FILE REFERENCE: ISIS0083-100 (BIO00080S)  
 ; CURRENT APPLICATION NUMBER: US/10/831,901A  
 ; CURRENT FILING DATE: 2004-04-26  
 ; PRIOR APPLICATION NUMBER: 60/466,426  
 ; PRIOR FILING DATE: 2003-04-28  
 ; PRIOR APPLICATION NUMBER: 60/468,562  
 ; PRIOR FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: 60/467,770  
 ; PRIOR FILING DATE: 2003-04-30  
 ; PRIOR APPLICATION NUMBER: 60/468,527  
 ; PRIOR FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: 60/477,637  
 ; PRIOR FILING DATE: 2003-06-10  
 ; PRIOR APPLICATION NUMBER: 60/483,579  
 ; PRIOR FILING DATE: 2003-06-27  
 ; NUMBER OF SEQ ID NOS: 30063  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 29740  
 ; LENGTH: 28920  
 ; TYPE: DNA  
 ; ORGANISM: SARS Coronavirus  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 7230-7329, 9929-10028, 10137-10216, 11646-11745, 20385-20484,  
 ; LOCATION: 2104-21123, 21753-21852, 22112-22211, 25301-25400  
 US-10-831-901A-29740

Query Match 90.9%; Score 20; DB 21; Length 28920;  
 Best Local Similarity 75.0%; Prod. No. 0.0089;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGACUCACUCCUGAGCUC 20  
 Db 776 GTGAACTCTACTCGTGAAGCTC 795

RESULT 13  
 US-10-889-101-5  
 ; Sequence 5, Application US/10889101  
 ; Publication No. US20050107324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bennett, C. Frank  
 ; APPLICANT: Dobie, Kenneth W.  
 ; APPLICANT: Jain, Ravi  
 ; TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION  
 ; FILE REFERENCE: ISIS0101-100 (RTS-0655US)  
 ; CURRENT APPLICATION NUMBER: US/10/889,101  
 ; CURRENT FILING DATE: 2004-07-12  
 ; PRIOR APPLICATION NUMBER: 60/486,652  
 ; PRIOR FILING DATE: 2003-07-12  
 ; NUMBER OF SEQ ID NOS: 238  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 5  
 ; LENGTH: 28920  
 ; TYPE: DNA

ORGANISM: SARS Coronavirus isolate BJ03  
 FEATURE: misc\_feature  
 LOCATION: n = A,T,C or G  
 OTHER INFORMATION: US-10-889-101-5

Query Match Score 20; DB 21; Length 28920;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Mismatches 0;

Qy 1 GUGAACUCACUCUGAGCUC 20  
 Db 776 GTGAACTACTCGTGTGTC 795

RESULT 14  
 US-10-889-101-6  
 Sequence 6, Application US/10889101  
 Publication No. US20050107324A1  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, C. Frank  
 APPLICANT: Doble, Kenneth W.  
 APPLICANT: Jain, Ravi  
 TITLE OF INVENTION: MODULATION OF CBACAM1 EXPRESSION  
 FILE REFERENCE: ISIS0101-100 (RTS-0655US)  
 CURRENT APPLICATION NUMBER: US/10/889,101  
 CURRENT FILING DATE: 2004-07-12  
 PRIOR APPLICATION NUMBER: 60/486,652  
 PRIOR FILING DATE: 2003-07-12  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 6  
 LENGTH: 28920  
 TYPE: DNA

ORGANISM: SARS Coronavirus isolate BJ04  
 FEATURE: misc\_feature  
 LOCATION:  
 OTHER INFORMATION: n = A,T,C or G

Query Match Score 20; DB 21; Length 28920;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Mismatches 0;

Qy 1 GUGAACUCACUCUGAGCUC 20  
 Db 776 GTGAACTACTCGTGTGTC 795

RESULT 15  
 US-10-889-101-6  
 Sequence 6, Application US/10889101  
 Publication No. US20050100885A1  
 GENERAL INFORMATION:  
 APPLICANT: Crooke, Stanley T.  
 APPLICANT: Ecker, David J.  
 APPLICANT: Sampath, Rangarajan  
 APPLICANT: Freier, Susan M.  
 APPLICANT: Massire, Christian  
 APPLICANT: Hofstader, Steven A.  
 APPLICANT: Lowery, Kristin Sannes  
 APPLICANT: Swazey, Eric  
 APPLICANT: Baker, Brenda F.  
 APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)  
 FILE REFERENCE: ISIS0083-100 (BIO008US)  
 CURRENT APPLICATION NUMBER: US/10/831,901A  
 CURRENT FILING DATE: 2004-04-26  
 PRIOR APPLICATION NUMBER: 60/466,426  
 PRIOR FILING DATE: 2003-04-28  
 PRIOR APPLICATION NUMBER: 60/468,562  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/467,770  
 PRIOR FILING DATE: 2003-04-30  
 PRIOR APPLICATION NUMBER: 60/468,627  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR FILING DATE: 2003-06-10  
 PRIOR APPLICATION NUMBER: 60/483,579  
 PRIOR FILING DATE: 2003-06-27  
 NUMBER OF SEQ ID NOS: 30063  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 29742  
 LENGTH: 29206  
 TYPE: DNA

ORGANISM: SARS Coronavirus  
 US-10-889-101-6

Query Match Score 20; DB 21; Length 29206;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCUGAGCUC 20  
 Db 776 GTGAACTACTCGTGTGTC 795

RESULT 16  
 US-10-831-901A-29742  
 Sequence 29742, Application US/10831901A  
 Publication No. US20050100885A1  
 GENERAL INFORMATION:  
 APPLICANT: Crooke, Stanley T.  
 APPLICANT: Ecker, David J.  
 APPLICANT: Sampath, Rangarajan  
 APPLICANT: Freier, Susan M.  
 APPLICANT: Massire, Christian  
 APPLICANT: Hofstader, Steven A.  
 APPLICANT: Lowery, Kristin Sannes  
 APPLICANT: Swazey, Eric  
 APPLICANT: Baker, Brenda F.  
 APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)  
 FILE REFERENCE: ISIS0083-100 (BIO008US)  
 CURRENT APPLICATION NUMBER: US/10/831,901A  
 CURRENT FILING DATE: 2004-04-26  
 PRIOR APPLICATION NUMBER: 60/466,426  
 PRIOR FILING DATE: 2003-04-28  
 PRIOR APPLICATION NUMBER: 60/468,562  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/467,770  
 PRIOR FILING DATE: 2003-04-30  
 PRIOR APPLICATION NUMBER: 60/468,627  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR FILING DATE: 2003-06-10  
 PRIOR APPLICATION NUMBER: 60/483,579  
 PRIOR FILING DATE: 2003-06-27  
 NUMBER OF SEQ ID NOS: 30063  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 29742  
 LENGTH: 29206  
 TYPE: DNA

ORGANISM: SARS Coronavirus  
 US-10-831-901A-29742

Query Match Score 20; DB 21; Length 29206;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCUGAGCUC 20  
 Db 776 GTGAACTACTCGTGTGTC 795

RESULT 17  
 US-10-831-901A-29819  
 Sequence 29819, Application US/10831901A  
 Publication No. US20050100885A1  
 GENERAL INFORMATION:  
 APPLICANT: Crooke, Stanley T.  
 APPLICANT: Ecker, David J.  
 APPLICANT: Sampath, Rangarajan  
 APPLICANT: Freier, Susan M.  
 APPLICANT: Massire, Christian  
 APPLICANT: Hofstader, Steven A.  
 APPLICANT: Lowery, Kristin Sannes  
 APPLICANT: Swazey, Eric  
 APPLICANT: Baker, Brenda F.  
 APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)  
 FILE REFERENCE: ISIS0083-100 (BIO008US)  
 CURRENT APPLICATION NUMBER: US/10/831,901A  
 CURRENT FILING DATE: 2004-04-26  
 PRIOR APPLICATION NUMBER: 60/466,426  
 PRIOR FILING DATE: 2003-04-28  
 PRIOR APPLICATION NUMBER: 60/468,562  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/467,770  
 PRIOR FILING DATE: 2003-04-30  
 PRIOR APPLICATION NUMBER: 60/468,627  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR FILING DATE: 2003-06-10  
 PRIOR APPLICATION NUMBER: 60/483,579  
 PRIOR FILING DATE: 2003-06-27  
 NUMBER OF SEQ ID NOS: 30063  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 29742  
 LENGTH: 29206  
 TYPE: DNA

ORGANISM: SARS Coronavirus  
 US-10-831-901A-29819

Query Match Score 20; DB 21; Length 29206;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCUGAGCUC 20  
 Db 776 GTGAACTACTCGTGTGTC 795

```

Db 751 GTGAACTCACTCGTGAGCTC 770
;
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6112_10070_10169, 10560, 10775, 10849_10948, 21378_21477, 22501,
; CURRENT APPLICATION NUMBER: US2005005307A1
; OTHER INFORMATION: n = A,T,C or G
; US-10-831-901A-29738

RESULT 17
; Sequence 4, Application US/10889447
; Publication No. US2005005307A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIORITY FILING DATE: 2003-07-12
; SEQ ID NO: 241
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
; US-10-889-44-4

Query Match 90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GUGAACUCACUCCUGAGCU 20
Db 726 GTGAACTCACTCGTGAGCTC 745

RESULT 18
; Sequence 29738, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstader, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swaye, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (B10100008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 29738
; LENGTH: 29291

RESULT 19
; Sequence 4, Application US/10889101
; Publication No. US2005010732A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
; FILE REFERENCE: ISIS0101-100 (RTS-065US)
; CURRENT APPLICATION NUMBER: US/10/889,101
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,652
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS Coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
; US-10-889-101-4

Query Match 90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GUGAACUCACUCCUGAGCU 20
Db 726 GTGAACTCACTCGTGAGCTC 745

RESULT 20
; Sequence 29739, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstader, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swaye, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (B10100008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 29738
; LENGTH: 29291

```



US-10-889-101-7      Query Match      90.9%; Score 20; DB 21; Length 29430;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Mismatches 0;

Qy      1      GUGAACUCUCCUGGAGCUC 20  
 Db      760      GTGAACTCTCGTGGAGTC 779

RESULT 24  
 US-10-831-901A-29802      Sequence 2802, Application US/10831901A  
 ; GENERAL INFORMATION:  
 ; Publication No. US20050100885A1.  
 ; APPLICANT: Crooke, Stanley T.  
 ; APPLICANT: Ecker, David J.  
 ; APPLICANT: Sampath, Rangarajan  
 ; APPLICANT: Freier, Susan M.  
 ; APPLICANT: Massire, Christian  
 ; APPLICANT: Hofstader, Steven A.  
 ; APPLICANT: Lowery, Kristin Sannes  
 ; APPLICANT: Swayze, Eric  
 ; APPLICANT: Baker, Brenda F.  
 ; APPLICANT: Bennett, C. Frank  
 ; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe  
 ; Acute Respiratory Syndrome (SARS)  
 ; FILE REFERENCE: IS1S0083-100 (BIO10008US)  
 ; CURRENT APPLICATION NUMBER: US/10/831,901A  
 ; CURRENT FILING DATE: 2004-04-26  
 ; PRIOR APPLICATION NUMBER: 60/446,426  
 ; PRIOR FILING DATE: 2003-04-28  
 ; PRIOR APPLICATION NUMBER: 60/446,562  
 ; PRIOR FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: 60/446,627  
 ; PRIOR FILING DATE: 2003-04-30  
 ; PRIOR APPLICATION NUMBER: 60/446,770  
 ; PRIOR FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: 60/446,737  
 ; PRIOR FILING DATE: 2003-06-10  
 ; PRIOR APPLICATION NUMBER: 60/448,579  
 ; PRIOR FILING DATE: 2003-06-27  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 29802  
 ; LENGTH: 29573  
 ; TYPE: DNA  
 ; ORGANISM: SARS Coronavirus  
 ; US-10-831-901A-29803

Query Match      90.9%; Score 20; DB 21; Length 29573;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Mismatches 0;

Qy      1      GUGAACUCUCCUGGAGCUC 20  
 Db      707      GTGAACTCTCGTGGAGTC 726

RESULT 26  
 US-10-831-901A-29807      Sequence 29807, Application US/10831901A  
 ; Publication No. US20050100885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Crooke, Stanley T.  
 ; APPLICANT: Ecker, David J.  
 ; APPLICANT: Sampath, Rangarajan  
 ; APPLICANT: Freier, Susan M.  
 ; APPLICANT: Massire, Christian  
 ; APPLICANT: Hofstader, Steven A.  
 ; APPLICANT: Lowery, Kristin Sannes  
 ; APPLICANT: Swayze, Eric  
 ; APPLICANT: Baker, Brenda F.  
 ; APPLICANT: Bennett, C. Frank  
 ; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe  
 ; Acute Respiratory Syndrome (SARS)  
 ; FILE REFERENCE: IS1S0083-100 (BIO10008US)  
 ; CURRENT APPLICATION NUMBER: US/10/831,901A  
 ; CURRENT FILING DATE: 2004-04-26  
 ; PRIOR APPLICATION NUMBER: 60/446,426  
 ; PRIOR FILING DATE: 2003-04-28  
 ; PRIOR APPLICATION NUMBER: 60/446,562  
 ; PRIOR FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: 60/446,627  
 ; PRIOR FILING DATE: 2003-04-30  
 ; PRIOR APPLICATION NUMBER: 60/446,770  
 ; PRIOR FILING DATE: 2003-05-06  
 ; PRIOR APPLICATION NUMBER: 60/446,737  
 ; PRIOR FILING DATE: 2003-06-10  
 ; PRIOR APPLICATION NUMBER: 60/448,579  
 ; PRIOR FILING DATE: 2003-06-27  
 ; NUMBER OF SEQ ID NOS: 30063  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 29807  
 ; LENGTH: 29573  
 ; TYPE: DNA  
 ; ORGANISM: SARS Coronavirus  
 ; US-10-831-901A-29802

Query Match      90.9%; Score 20; DB 21; Length 29573;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Mismatches 0;

Qy      1      GUGAACUCUCCUGGAGCUC 20  
 Db      707      GTGAACTCTCGTGGAGTC 726

RESULT 25  
 US-10-831-901A-29803      Sequence 29803, Application US/10831901A  
 ; Publication No. US20050100885A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Crooke, Stanley T.  
 ; APPLICANT: Ecker, David J.  
 ; APPLICANT: Sampath, Rangarajan  
 ; APPLICANT: Freier, Susan M.  
 ; APPLICANT: Massire, Christian  
 ; APPLICANT: Hofstader, Steven A.  
 ; APPLICANT: Lowery, Kristin Sannes  
 ; APPLICANT: Swayze, Eric  
 ; APPLICANT: Baker, Brenda F.

RESULT 27  
 US-10-831-901A-29820  
 Query Match 90.9%; Score 20; DB 21; Length 29573;  
 Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 5; Indels 0; Gaps 0;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NOS: 30063  
 Qy 1 GUGAACUCACUGGAGCUC 20  
 Db 707 GTGAACTACTCGTGAAGTC 726

RESULT 28  
 US-10-831-901A-29820  
 Sequence 29820, Application US/10831901A  
 PUBLICATION NO. US2005100885A1  
 GENERAL INFORMATION:  
 APPLICANT: Crooke, Stanley T.  
 APPLICANT: Ecker, David J.  
 APPLICANT: Sampath, Rangarajan  
 APPLICANT: Freier, Susan M.  
 APPLICANT: Massire, Christian A.  
 APPLICANT: Hofstadler, Steven A.  
 APPLICANT: Lowery, Kristin Sannes  
 APPLICANT: Swazye, Eric  
 APPLICANT: Baker, Brenda F.  
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)  
 FILE REFERENCE: ISIS0083-100 (BIOL0008US)  
 CURRENT APPLICATION NUMBER: US/10/831,901A  
 CURRENT FILING DATE: 2004-04-26  
 PRIOR APPLICATION NUMBER: 60/466,426  
 PRIOR FILING DATE: 2003-04-28  
 PRIOR APPLICATION NUMBER: 60/468,562  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/467,770  
 PRIOR FILING DATE: 2003-04-30  
 PRIOR APPLICATION NUMBER: 60/468,627  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR FILING DATE: 2003-06-10  
 PRIOR APPLICATION NUMBER: 60/483,579  
 PRIOR FILING DATE: 2003-06-27  
 NUMBER OF SEQ ID NOS: 30063  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 29758  
 LENGTH: 29705  
 TYPE: DNA  
 ORGANISM: SARS Coronavirus  
 US-10-831-901A-29758

RESULT 29  
 US-10-831-901A-29791  
 Sequence 29791, Application US/10831901A  
 Publication No. US2005100885A1  
 GENERAL INFORMATION:  
 APPLICANT: Crooke, Stanley T.  
 APPLICANT: Ecker, David J.  
 APPLICANT: Sampath, Rangarajan  
 APPLICANT: Freier, Susan M.  
 APPLICANT: Massire, Christian A.  
 APPLICANT: Hofstadler, Steven A.  
 APPLICANT: Lowery, Kristin Sannes  
 APPLICANT: Swazye, Eric  
 APPLICANT: Baker, Brenda F.  
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)  
 FILE REFERENCE: ISIS0083-100 (BIOL0008US)  
 CURRENT APPLICATION NUMBER: US/10/831,901A  
 CURRENT FILING DATE: 2004-04-26  
 PRIOR APPLICATION NUMBER: 60/466,426  
 PRIOR FILING DATE: 2003-04-28  
 PRIOR APPLICATION NUMBER: 60/468,562  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/468,627  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/468,627  
 PRIOR FILING DATE: 2003-05-06  
 PRIOR APPLICATION NUMBER: 60/477,637  
 PRIOR FILING DATE: 2003-06-10  
 PRIOR APPLICATION NUMBER: 60/483,579  
 PRIOR FILING DATE: 2003-06-27  
 NUMBER OF SEQ ID NOS: 30063  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 29820  
 LENGTH: 29592  
 TYPE: DNA  
 ORGANISM: SARS Coronavirus  
 US-10-831-901A-29820

RESULT 28  
 US-10-831-901A-29758  
 Sequence 29758, Application US/10831901A  
 Publication No. US2005100885A1  
 GENERAL INFORMATION:  
 APPLICANT: Crooke, Stanley T.  
 APPLICANT: Ecker, David J.  
 APPLICANT: Sampath, Rangarajan  
 APPLICANT: Freier, Susan M.  
 APPLICANT: Massire, Christian A.  
 APPLICANT: Hofstadler, Steven A.  
 APPLICANT: Lowery, Kristin Sannes

;

;

TYPE: DNA  
ORGANISM: SARS Coronavirus  
us-10-831-901A-29791

Query Match 90.9%; Score 20; DB 21; Length 29705;  
Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 5; Indels 0; Gaps 0;  
Matches 15; Conservative

Qy 1 GUGAACUCACUCCUGAGCTC 20  
Db 760 GTGAACTACTCGTGAAGCTC 779

---

RESULT 30

US-10-831-901A-29756

Sequence 29756, Application US/10831901A  
Publication No. US20050100885A1.

GENERAL INFORMATION:

APPLICANT: Crooke, Stanley T.  
APPLICANT: Ecker, David J.  
APPLICANT: Sampath, Rangarajan  
APPLICANT: Freier, Susan M.  
APPLICANT: Massire, Christian  
APPLICANT: Hofstader, Steven A.  
APPLICANT: Lowery, Kristin Sannes  
APPLICANT: Swayze, Eric  
APPLICANT: Baker, Brenda F.  
APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe  
TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)

FILE REFERENCE: 1STUS083-100 (B10L00080S)

CURRENT APPLICATION NUMBER: US/10/831,901A  
CURRENT FILING DATE: 2004-04-26

PRIOR APPLICATION NUMBER: 60/466,426  
PRIOR FILING DATE: 2003-04-28

PRIOR APPLICATION NUMBER: 60/468,562  
PRIOR FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: 60/467,770  
PRIOR FILING DATE: 2003-04-30

PRIOR APPLICATION NUMBER: 60/468,627  
PRIOR FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: 60/477,637  
PRIOR FILING DATE: 2003-06-10

PRIOR APPLICATION NUMBER: 60/483,579  
PRIOR FILING DATE: 2003-06-27

NUMBER OF SEQ ID NOS: 30063  
SOFTWARE: FastSEQ For Windows Version 4.0  
SEQ ID NO: 29756  
LENGTH: 29706

TYPE: DNA  
ORGANISM: SARS Coronavirus

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 20688  
OTHER INFORMATION: n = A,T,C or G

US-10-831-901A-29756

Query Match 90.9%; Score 20; DB 21; Length 29706;  
Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 5; Indels 0; Gaps 0;  
Matches 15; Conservative

Qy 1 GUGAACUCACUCCUGAGCTC 20  
Db 760 GTGAACTACTCGTGAAGCTC 779

Search completed: July 21, 2005, 01:08:21  
Job time : 609 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	20	90.9	1706	14 AY322205\$1	AY322205 SARS coro
2	20	90.9	14011	14 AY534758\$1	AY534758 SARS coro
3	20	90.9	26333	14 AY286320	AY286320 SARS coro
4	20	90.9	29013	14 AY461060	AY461060 SARS coro
5	20	90.9	29350	14 AY394999	AY394999 SARS coro
6	20	90.9	29350	14 AY395000	AY395000 SARS coro
7	20	90.9	29350	14 AY395001	AY395001 SARS coro
8	20	90.9	29350	14 AY395002	AY395002 SARS coro
9	20	90.9	29433	14 AY394977	AY394977 SARS coro
10	20	90.9	29530	14 AY394985	AY394985 SARS coro
11	20	90.9	29573	14 AY338174	AY338174 SARS coro
12	20	90.9	29573	14 AY338175	AY338175 SARS coro
13	20	90.9	29573	14 AY343114	AY343114 SARS coro
14	20	90.9	29577	14 AY550904	AY550904 SARS coro
15	20	90.9	29592	14 AY463059	AY463059 SARS coro
16	20	90.9	29620	14 AY394904	AY394904 SARS coro
17	20	90.9	29640	14 AY394978	AY394978 SARS coro
18	20	90.9	29645	14 AY394979	AY394979 SARS coro
19	20	90.9	29646	14 AY394982	AY394982 SARS coro

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score	Match	Length	DB	ID	Description
71	72	90.9	29729	14 AY502927	SARS coro
73	74	90.9	29729	14 AY502928	SARS coro
74	75	90.9	29729	14 AY502929	SARS coro
75	76	90.9	29729	14 AY502930	SARS coro
76	77	90.9	29729	14 AY502931	SARS coro
77	78	90.9	29729	14 AY502932	SARS coro
78	79	90.9	29729	14 AY502933	SARS coro
79	80	90.9	29732	14 AY279354	SARS coro
80	81	90.9	29733	14 AY508724	SARS coro
81	82	90.9	29733	14 AY294984	SARS coro
82	83	90.9	29736	14 AY278554	SARS coro
83	84	90.9	29736	14 AY282752	SARS coro
84	85	90.9	29736	14 AY245986	SARS coro
85	86	90.9	29736	14 AY245987	SARS coro
86	87	90.9	29736	14 AY245988	SARS coro
87	88	90.9	29736	14 AY294989	SARS coro
88	89	90.9	29736	14 AY394990	SARS coro
89	90	90.9	29736	14 AY394991	SARS coro
90	91	90.9	29736	14 AY394992	SARS coro
91	92	90.9	29736	14 AY394993	SARS coro
92	93	90.9	29736	14 AY394998	SARS coro

93	20	90.9	29738	14	AY350750	SARS	coro	c	166	15	68.2	12050	10	MNGU575748	
94	20	90.9	29738	14	AY350755	SARS	coro	c	167	15	68.2	43599	9	HSU15177	
95	20	90.9	29740	14	AY278490	SARS	coro	c	168	15	68.2	50389	1	AE014137	
96	20	90.9	29740	14	AY1310120	SARS	coro	c	169	15	68.2	51430	2	AC014137	
97	20	90.9	29740	14	AY485278	SARS	coro	c	170	15	68.2	54668	6	AX602203	
98	20	90.9	29741	14	AY204486	SARS	coro	c	171	15	68.2	61524	9	AL353725	
99	20	90.9	29741	14	AY485277	SARS	coro	c	172	15	68.2	81786	9	AC003002	
100	20	90.9	29742	14	AY278491	SARS	coro	c	173	15	68.2	83369	8	ATM30A1	
101	20	90.9	29745	14	AY278487	SARS	coro	c	174	15	68.2	98412	8	AC007187	
102	20	90.9	29745	14	AY57076	SARS	coro	c	175	15	68.2	110000	1	CP00003_01	
103	20	90.9	29745	14	AY654624	SARS	coro	c	176	2	68.2	110000	2	AC110967_2	
104	20	90.9	29749	14	AY51680	SARS	coro	c	177	15	68.2	140012	8	AC135500	
105	20	90.9	29751	14	AY274119	SARS	coro	c	178	15	68.2	143050	1	SAG76843	
111	20	90.9	29765	14	AY394994	SARS	coro	c	184	15	68.2	156692	2	CR356245	
112	20	90.9	29767	14	AY59083	SARS	coro	c	185	15	68.2	160950	1	AC011849	
113	17	77.3	147433	2	AC137257	Rattus	no	c	186	15	68.2	162105	5	BX001032	
c	114	17	77.3	156564	2	AC120103	Rattus	no	c	187	15	68.2	162342	2	AC132755
c	115	16	72.7	221722	2	AC10567	Rattus	no	c	188	15	68.2	162363	2	AC121352
c	116	16	72.7	838	2	AK052203	Oryza	sat	c	189	15	68.2	164000	9	AL591682
c	117	16	72.7	947	8	AK099574	Oryza	sat	c	190	15	68.2	164766	10	AC144792
c	118	16	72.7	120551	9	AY23977	SARS	coro	c	191	15	68.2	174839	8	AL157395
c	119	16	72.7	127267	9	AY313906	SARS	coro	c	192	15	68.2	184783	8	AC136972
c	120	16	72.7	158563	2	AC150484	Bos	tauru	c	193	15	68.2	188901	2	AC132886
c	121	16	72.7	176629	2	AC155792	Homo	sapi	c	194	15	68.2	189318	2	CR376821
c	122	16	72.7	218200	2	AC141165	Rattus	no	c	195	15	68.2	189757	3	AC008186
c	123	16	72.7	227026	2	AC136659	Rattus	no	c	196	15	68.2	190708	9	AC005261
c	124	16	72.7	237554	2	AC114189	Rattus	no	c	197	15	68.2	191928	10	AC138714
c	125	16	72.7	238390	2	AC117035	Rattus	no	c	198	15	68.2	198116	10	AC130217
c	126	16	72.7	238394	2	AC131227	Rattus	no	c	199	15	68.2	199754	8	ATCHRV26
c	127	16	72.7	247089	2	AC151695	Mus	muscu	c	200	15	68.2	201072	2	AC130278
c	128	15	68.2	534	6	CQ649388	Sequence	c	201	15	68.2	204168	10	AC147989	
c	129	15	68.2	537	6	AK607323	Sequence	c	202	15	68.2	206615	15	AC139041	
c	130	15	68.2	627	6	AX593704	Sequence	c	203	15	68.2	206967	10	AC007786	
c	131	15	68.2	1009	10	AF084464	Rattus	no	c	204	15	68.2	210344	9	AC007100
c	132	15	68.2	1794	10	BC018219	Mus	muscu	c	205	15	68.2	219750	2	AC110957
c	133	15	68.2	1820	6	CQ057040	Sequence	c	206	15	68.2	220175	2	AC114835	
c	134	15	68.2	1820	6	CQ076301	Sequence	c	207	15	68.2	227774	2	AC123156	
c	135	15	68.2	1870	6	CQ107294	Sequence	c	208	15	68.2	229061	9	AC007786	
c	136	15	68.2	1870	6	CQ184142	Sequence	c	209	15	68.2	229061	2	AC074163	
c	137	15	68.2	1870	6	CO205753	Sequence	c	210	15	68.2	232401	2	AC106137	
c	138	15	68.2	1870	6	CO267291	Sequence	c	211	15	68.2	233788	2	AC10957	
c	139	15	68.2	1870	6	CQ304315	Sequence	c	212	15	68.2	240107	2	AC126997	
c	140	15	68.2	1870	6	CQ341583	Sequence	c	213	15	68.2	243313	3	AC130104	
c	141	15	68.2	1870	6	CQ078257	Sequence	c	214	15	68.2	243313	3	AE003834	
c	142	15	68.2	1870	6	CQ109247	Sequence	c	215	15	68.2	245066	2	AC094644	
c	143	15	68.2	1870	6	CQ147884	Sequence	c	216	15	68.2	252411	2	AC094615	
c	144	15	68.2	1870	6	CQ183233	Sequence	c	217	15	68.2	256781	2	AC097952	
c	145	15	68.2	1870	6	CQ207657	Sequence	c	218	15	68.2	260227	2	AC150660	
c	146	15	68.2	1870	6	CQ269291	Sequence	c	219	15	68.2	261031	2	AC140768	
c	147	15	68.2	1870	6	CQ269291	Sequence	c	220	15	68.2	270221	2	AC107500	
c	148	15	68.2	1870	6	CQ343438	Sequence	c	221	15	68.2	277296	2	AC133556	
c	149	15	68.2	1966	6	CO052020	Sequence	c	222	15	68.2	311600	1	AP05141	
c	150	15	68.2	1966	6	CQ328817	Sequence	c	223	14	63.6	428	6	AR04034	
c	151	15	68.2	1966	6	CQ094118	Sequence	c	224	14	63.6	428	6	AR519316	
c	152	15	68.2	1966	6	CQ171485	Sequence	c	225	14	63.6	488	12	AY200782	
c	153	15	68.2	1966	6	CQ269291	Sequence	c	226	14	63.6	534	6	CO649386	
c	154	15	68.2	1966	6	CQ254675	Sequence	c	227	14	63.6	590	11	AL035144	
c	155	15	68.2	1966	6	CQ291760	Sequence	c	228	14	63.6	788	11	BV032952	
c	156	15	68.2	1966	6	CQ328817	Sequence	c	229	14	63.6	819	11	BV014760	
c	157	15	68.2	3066	8	AK110007	Oryza	sat	c	230	14	63.6	1081	9	HSIA28315
c	158	15	68.2	4064	6	CQ572246	Sequence	c	231	14	63.6	1142	9	HSIA32579	
c	159	15	68.2	4064	6	CQ574070	Sequence	c	232	14	63.6	1143	6	AF033649	
c	160	15	68.2	4089	6	CQ576314	Sequence	c	233	14	63.6	1341	6	AO51735	
c	161	15	68.2	4317	9	HSIA276316	Romo	sapi	c	234	14	63.6	1341	8	AF058905
c	162	15	68.2	8842	2	AC131316	Rattus	no	c	235	14	63.6	1347	8	BT008754
c	163	15	68.2	11518	10	MMU011265	Mus	muscu	c	237	14	63.6	1497	3	AF083644
c	164	15	68.2	11570	1	AE009595	Streptoco	c	238	14	63.6	1514	8	AY099805	
c	165	15	68.2	12028	1	AE006478	Streptoco	c	238	14	63.6	1539	3	AF083643	

卷之三

SOURCE	1 of 4 coronaviruses
ORGANISM	SARS coronavirus Sinf049
VIRUSES:	SARS coronavirus Sinf049
REFERENCE	1 (bases 1 to 1400)
AUTHORS	Lim, P.L., Kurup, A., Gopalakrishna, G., Chan, K.P., Wong, C.W.,

Ng, L.C., Se-Thee, S.Y., Oon, L., Bai, X., Stanton, L.W., Ruan, Y., Miller, L.D., Vega, V.B., James, J., Ooi, P.L., Kai, C.S., Olsen, S.J., Ang, B. and Leo, Y.S.	REFERENCE Authors Wang, Z., Cheng, S. and Zhang, Y. Title Direct Submission Journal Submitted (17-DEC-2003) Department of Microbiology, Zhejiang CDC, 17 Laozhedzhi Rd., Hangzhou, Zhejiang 310000, China
JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	REMARK COMMENT On Dec 17, 2003 this sequence version replaced gi:38304880. Location/Qualifiers 1. .26333 /organism="SARS coronavirus ZJ01" /mol_type="genomic RNA" /isolate="ZJ01b" /isolation_source="cultured virus in Vero cell inoculated with throat swab from patient with severe acute respiratory syndrome (SARS)" /db_xref="Taxon:230471" /country="China: Hangzhou" /note="isolated April 21, 2003" 1. .248 5' UTR mi sc_feature CDS /transcription regulatory sequence leader; TRS" join(249 ..13382,13382 ..21469) /note="ribosomal slippage" /codon_start=1 /product="orf lab polyprotein" /protein_id="AAH49011_4" /db_xref="GI: 38324306" /translation="MESIVLGVNNEVTHVQLPVLQVGDYVLRGFDVSBEALSEARE HLKNGNCGLPLEKGSIPOLEQPVYFVKPSDALSINHGKVWVLAEMDGIVQGSQI TLGVLPVPHGSPTPAVRNVLQKNGKGAGHSYSGIDLKSTYDGLDGEIDEYEQN WNTKRGSGAARELTRELNGGAUTYDNFGCPDGYPLDCKDADKFLARAGSMTCPTKEVUP LDYIERSKGTYCCRDEHEIATWERTSYEHOHPPTRELSKYEYDTEKCPKCNHDEBVSQTC LNSKVKVIAQPVBRKKTGFMGRISVYPPASQPCENMHULSTLMKCNHDEBVSQTC DLFRATCEHCCTENLIVIEGTGPTCGYLPTNAVKMPCACDPEPEHASYDVETNLHN IETRLRKGPTRCEGGCFVAYVGYNKRATVWPRASADISGHTGTTGDNVETNLHN LEILSRSERVNINIVGDPFHNLBEVALLASPAASATSAFDITKLSDYKSKTIVESCN YKVTKRGPKVGAWNICQORSSVYTLPGEPFQVYVQAGVIRSPARTLQVTSN VTLIDGISEQSRLVUDAMVYTSQDILQVQTSOMSNLIGTVEKL RPFWIEKAUSAGVFLQDWEILKPLTGFVDLVQQLQVASDNIKDCVKFCFIDVV NKALENCIDQVTIAGAKLRSNLQGEGVFLAQSKGLYRCQGKEQOLIMPQKAEVKET FLEGOSHDTWLTSEEVNLKNGELEALETPTDSDFTGAVLVEYTPVCGVQMLMIEIKO YCALSPGLATINVRKGGAPAKIGVTFGBDWTWVQGNVRVTFLLDVERDKUNA KC5VYTVESGTEVTEFAVVAEEVYKPTDCEUTMNGIDDENVATPFLLD ENFSRSMYCSYPDDEBEDDAECCEDIEDETCYDQSYPLFEGASAATV VEEEBDWLDTTBSELEPE NPMTVIAANTHLKRGGGVAGALNATNGAKMOKSDFKINGPLVGGSCLLSGHNL AKKCHVVGPNLNASEDIOILQKKAVENTNGAKMOKSDFKINGPLVGGSCLLSGHNL VRTQVIAVNDKALYEQWMDLNUKRYVEAPQEPPNTEDSKTEKSNUVKPVD VGDVTSQDGTICVWVLPSKRAGGTTEMLSLALKVVDYVPEPEPEPEPEPEPEPEPE ALKKCKSAFVYLPSEPNKABEELGTVSWNLREMLAHAETRKLMPICMODVRAIMATI ORKYKGKIQIGIVDGVRFFFYTSKEPQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQ EAARCNRSLRKAPEVSYVSPPDAVITYNGUTTSKTSSEHEVETVSLAGSYTSRDWSYSG ORTLGEGEELKRGDKIVWHLESPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE NTNLNLTQVDMSTYQQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQ YHTLDESPLGURMSYQALNPHKWKWPQVGGGTSKWDNNCYLSVLLALQOLEVKFN APALQRAYRRAQDANECALLAYSNKTVGELEDVREPMTHLQHNLSEAKWVN VWCHRGQKQTTLTGVBAYMGMQPLVMPVLTQGVSIPCVCEPDTQWSSFWM SAPPAYKQLOGTGFICANEYTQNYOGCHHTITAKETLYLSDGAHILTMKSYKGPVTD CAKRLQAVENYMPVYTFMILLFOLCFTKTSNTRASPLPTIAKNSVSKVAKLCLDA GINYUKSPKSKLEFTLAMMILLISCLGSLICVTAQGVLISNEAPSYCNGVREYL VEYKETSYTITKPKSYKLCVTPKPAKDLNQNTGTPKPAKSLVTPKPAKSLVTPKPA SFDNFLKTCSTSNTKPAKDLNQNTGTPKPAKSLVTPKPAKSLVTPKPAKSLVTPKPA GAKLJHKPQWUHINOATTKUTKPKPTWCLMSTKPKVDTNSFEVATEBTQMDNL ACESQOPTSEEVNVENTIQKEVIECDVYKTOEGLHEDIMA AYVENTSITKPKNEUSLALGKLTQHGNIAINSTWPSKLLAYVPLQGVSIPCVCEPDTQWSSFWM CAKRLQAVENYMPVYTFMILLFOLCFTKTSNTRASPLPTIAKNSVSKVAKLCLDA GINYUKSPKSKLEFTLAMMILLISCLGSLICVTAQGVLISNEAPSYCNGVREYL NSNNTMIDFCGSPCISLGSFPCISLGSFPCISLGSFPCISLGSFPCISLGSFPC AYMLFTKFKFVYLLGSLAISMOVPGYFASHFESNSWLMWELISIVQAPVSAVMYTF ASFYIYIKWSYTHIMDGCTSTCMCMYKRNATRVCETVINGMKSFYVYANGGRFC YDKAGQKTYERHPUSHPVNLDRANNTGSPLPNVTFGSKSCDEASAKSASYL SOLMCOPILLDOALJSDVSESTEVSVMMDAYDTEFSAFSEVPMEKJKLVALVATAHSE LAKGVADLGVLSTFVSARQSVVDTDVTDVIECILKSHSDEVTGDSCNMFYLI
Query Match Best Local Similarity Matches 15% 1. .14011 /organism="SARS coronavirus Sis0409" /mol_type="genomic RNA" /db_xref="Taxon:266147" /country="Singapore"	RESULT 3 LOCUS AY286320 DEFINITION SARS coronavirus ZJ01, partial genome. ACCESSION AY286320 VERSION AY286320..4 KEYWORDS SOURCE ORGANISM SARS coronavirus ZJ01 Viruses; SARS positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus. (bases 1 to 26333) Li, L., Wang, Z., Lu, Y., Bao, Q., Chen, S., Wu, N., Cheng, S., Weng, J., Zhang, Y., Yan, J., Mai, L., Wang, X., Zhu, H., Yu, Y., Zhang, M., Li, M., Yao, J., Lu, Q., Yao, P., Bo, X., Wo, J., Wang, S. and Hu, S. TITLE Severe acute respiratory syndrome-associated coronavirus genotype and its characterization JOURNAL Chin. Med. J. 116 (9), 1288-1292 (2003) MBIDLINE 22889812 PUBMED 14527350 REFERENCE 2 (bases 1 to 26333) AUTHORS Wang, Z.G., Li, L.J., Luo, Y., Zhang, J.Y., Wang, M.Y., Cheng, S.Y., Zhang, Y.J., Wang, X.M., Lu, Y.Y., Wu, N.P., Mei, L.L. and Wang, Z.X. TITLE Molecular biological analysis of genotyping and phylogeny of severe acute respiratory syndrome associated coronavirus JOURNAL Chin. Med. J. 117 (1), 42-48 (2004) PUBMED 14733731 REFERENCE 3 (bases 1 to 26333) AUTHORS Wang, Z., Cheng, S. and Zhang, Y. TITLE Direct Submission JOURNAL Submitted (19-JUN-2003) Department of Microbiology, Zhejiang CDC, 17 Laozhedzhi Rd., Hangzhou, Zhejiang 310009, China REFERENCE 4 (bases 1 to 26333) AUTHORS Wang, Z., Cheng, S. and Zhang, Y. TITLE Direct Submission JOURNAL Submitted (13-NOV-2003) Department of Microbiology, Zhejiang CDC, 17 Laozhedzhi Rd., Hangzhou, Zhejiang 310009, China REFERENCE 5 (bases 1 to 26333) AUTHORS Wang, Z., Cheng, S. and Zhang, Y. TITLE Direct Submission JOURNAL Submitted (13-NOV-2003) Department of Microbiology, Zhejiang CDC, 17 Laozhedzhi Rd., Hangzhou, Zhejiang 310009, China REFERENCE 6 (bases 1 to 26333) AUTHORS Wang, Z., Cheng, S. and Zhang, Y. TITLE Direct Submission JOURNAL Submitted (17-DEC-2003) Department of Microbiology, Zhejiang CDC, 17 Laozhedzhi Rd., Hangzhou, Zhejiang 310009, China



VEEEEDWLDDETEOSIEPEPEPTPEPEPNQFTGYKLTDNAIKCVDTYKEAQSA  
NPMVTAANHTHKGAGGATKNGAMQESDITLKLPGSCLLUSQVYNT  
AKKCHUVGPNLNAGEDDOLKKAAYENFNSODILLAPLPSAIGFPLGOSLUQCVYNT  
VPTQVYI AUNDKALYEQMNDLNPRAVEAKQEEPNTEDSKTEKSUOKVPUV  
KPKTACIDTCVTPKLTNLKFLDINGLHYSSQMLNRGFLSFLBZDPM  
WGDVTSQGDTCTVTPKLTNLKFLDINGLHYSSQMLNRGFLSFLBZDPM  
ALKICKSAFTVPLSEAPIAKEILGUTSVNIRLEMIAHEARLKMPICMDVRAIMATI  
ORQARYCKMSKIAPOVASYSPDAVTYNGUTSSEKTSSEHVFYUTVAGSWSLSSG  
ORTELGEVELKRGDKVTHITLESPLTPEFLDGEVLSLICKSLSLRETKTIVFTV  
NTYLTDQLVDMSSMTAALNPKWNEKPKWNEKPKWNEKPKWNEKPKWNE  
APALQEA YFRAQDAA NF CALLAISXKTVGEJUDVBTMTHLQRANLBSKRVIN  
VVKCHGKPLTGTCEVANMVTGNGOYQHGTTAKEYETRIDGAHLMSTKXGPNT  
WVYETS WTI KPV YKLGDVTVTEBKPLDGYKDNAYVENTSITIKRNELSLA  
LGLFOLCUTETESTNSRIRASPLTAKUNSKVAKLUGAGINXVSYKPT  
LLLSLGSLI CTAFAFGTLLSNFGAPSYCNGTRFLTLNSAATNTMDCBGSFPCST  
CLSGSDLSDESYPALETTQVITISYKLDTLGMALYTAEWWLYMLTFKPTVYLGMSLA  
AEGFQFASHSTNSNMMPLTISIVSYKPTVYLGMSLA MOQ  
STCMCKCNHATRBCITVNGMRSFVYANGRGFCRTHWNCLCDTCTGSTP  
ISDEVARDLISLQKRPINPDDQSSIVDVAENGALYPFDRAGQKTYERBLPSHF  
NDUNRANPQKSPINPNTYQDSSKQVYKPTVYLGMSLA  
GDSTEVSKRFDAVDTSATSYPSVMEKULAVATAHBBLARGVALDQVLSTVSAAR  
QHINQAVAKSHSI IMMYKHDYNSLQSRQKPSRQKAKKNNPBRPLTGACTPQVNUV  
TTKSLKQKLVSTCPKMLKATLCLVCLALVCYVMMVHUTLISHDGTNELEYKAI  
ODGTWRDITSTDQPKRQHADFWSSORGSSKNDKRCPSVYAIITREIGFVPGLP  
PVPYCZTNDLLEGPSYSEASIGNKPSKLLSESPATSAVNCETIENDAKC  
GTCCESEVGICLSTSGRWVUNNENHYRALSGVFCGVDANLNLANIETPLVOPVYALDAS  
GQVWDQDVTDKDVTCBLKLSHSDLEVTGDSYCNYTMVNTMPLDLAGCITCNVA  
ASVNGTALALJTCAYKEMMPSVYKPTVYLGMSLA  
LKRKMUNGTYPSPEBEAALCTFLKMKYKURSETTELPLTQDYNRYALXNKYKTES  
EGWVQYVTFYFTFDNSFLAHQWQFAMPSVTPFWMFTAIVFCISLKHCFWV  
ROTAQAGDTTITLNLAWL YAATVNGDRWFNLRTTDLNDVANKTBLPTD  
HVDLGLPSLKGHTGAVLNDCAALKEBLONGMNGTRTLLGTTTDEPFDVYRQCS  
TFLQKRGPSLKGHTGAVLNDCAALKEBLONGMNGTRTLLGTTTDEPFDVYRQCS  
AMLYVRKHAFLCLLPSLATVAYNNTYMPASWVRIIMTWBLADLSSEGRVYKTA  
VMSAISQVUTTILMARTDAAVRWVTLWNTVLYKQYVYQVYALDQDLSA  
TNSYSGCVUTTILMARTDAAVRWVTLWNTVLYKQYVYQVYALDQDLSA  
LLNRYRTRLGVDYDYLSTOFTRMNSQBLPPKSIAUAFKINLKLIGGGPCKIVKA  
TQVSOMSIVDCTSVLVSLVQORVYESSRLLQVYQYPLFENTLQTMUNIYCEGK  
SEVBUKQKSLAYAKSEPDRLAMQKLRKQADQMTQYKCARSEKRAVTSAMQ  
TMLFTMLRLKDNDLANNLNNARQCVPINLUTTAKALMVTYVDPYCTQKNTCDNT  
FVYASALWBLWQDQDLSKIVQSLVSEIIMDNLPLJLTAQKQNLONNSLSP  
VALRONSACAGTQADTCDNALLAYNNKGRTFLAULJSRDLKWAVERPKSDGTT  
IYTELEPPCPFUTDPKGPKMVLFYFIGLANNLRGMVGLGSLAATVRLQAGNATEPA  
NSTVSLQKSLAYAKSEPDRLAMQKLRKQADQMTQYKCARSEKRAVTSAMQ  
FVGASGSCCLYCRDHDPNGFCGDFQKTYQVTOIPCTQIATVTPAMDQCS  
YGCSCDQDLREPLMOSADESTEPRKVCGSAARLTPCCGTSTDNTVADTINKEVAG  
PFAKLTKNCRQFQEADLWVQFQVNGPQKDFDFAVSYKPTVYLGMSLA  
KFRVGDYDMPHISORLTYKTMADLYRHLDFDENGTCITKELIUYTNCDDYFRNK  
DWYDVEVNPDLRUYANLBRVROSLLKTYQEDAMRAGIVSLTDNODLANGNMYY  
WGKARLYXDSMSYEBODALFAYTERVNPTITOMNLKTAISAGNRACTVAGSICSM  
TNPQRQHQLKSLAYAKSEPDRLAMQKLRKQADQMTQYKCARSEKRAVTSAMQ  
AMPNKLINIASLVRKQNTCCLNUSLHTRBLANEQVPLFVTPPSPLVURKPL  
GDATTAYANSVENICONTANVNLALSDTGCKLADKVTNTQHRLYCYLZNRDVDEH  
WDFEFTAYLRKHFMSWVLSLSDAVVQCNHSDNLSKFLVYADPAMHASNGLDQR  
CWTDETDLQPSQPSQPSQPSQPSQPSQPSQPSQPSQPSQPSQPSQPSQPSQ  
ERFVSLAIDYPLTCHPQNEYADYHFLXQVYDQVYDQVYDQVYDQVYDQVYDQVY  
WWEPEY AYVTPHLLQVYDQVYDQVYDQVYDQVYDQVYDQVYDQVYDQVYDQVY  
LVLSTNQYXQNAQGDPVYDQVYDQVYDQVYDQVYDQVYDQVYDQVYDQVYDQVY  
TNPQRQHQLKSLAYAKSEPDRLAMQKLRKQADQMTQYKCARSEKRAVTSAMQ  
TNPQRQHQLKSLAYAKSEPDRLAMQKLRKQADQMTQYKCARSEKRAVTSAMQ

S  
8

20834 . 24601  
/codon\_start=1  
/product = "spike"  
/protein\_id="P86775\_1"  
/db\_xref="IGI:1045750"  
/translation="MFIFLFLITLTSGSILDRCCTTFFDDVQAPNTQTQHTSSMRGVYYPD  
EFGSTMNNKKSOSVLLNFSNTNVVACNPFELCDNODFPPFKPDKMGTOTHTMILDNFAFNCT  
FEYISDAFSLDVSEKSGNKHRLREFPKNDGLFLVYKGQIDVVRDPSGNTLKE  
IKFGLPQINMLNRAILTFSPAQDIOWTGNGVYPPGDFVYPPNTLNQCGEVENATKPF  
DCSONPLAEEKCSKSFEDKGTYTQNSRNRVPGDQVYPPNTLNQCGEVENATKPF  
PSVTAWERKKISNCVADSYLVNSTFESTFKCQGYUSATCCLDQPSNVAADSFLVKGQ  
DVRQAGPQGTVVADYNYKLPPDQCNWPLDQVYPPNTLNQCGEVENATKPF  
FDRDLSNVSPEPDGKPTPALNCYWPFLDQVYPPNTLNQCGEVENATKPF  
TVCGPKLSDTLIRNOQUNNENGLTGTLTPSSSKRFQFOQFRDVSPTDSVSDPK  
TSEBLIDSPCAQGKQSVTITGTTNASEAVLYQDNCNTVSAHADQPLAUYST  
GNNYQTOACCLIGAEHWTSYCEPDIAGIICASHTYSLRSRSTSKQVAYTMSLG  
ADSSAYSNNTIAPTNEFSLISITEVNPMSAKTSVDCMYLCDSSTEANLQIYQGS  
FCTQINRQHSDREVAQDINRQKIPITKLYFGNFNQKGLDPLKFTRS  
FIEDLFLNVTLLADGMKQYGECDINARLDIACQAGLQVYPPNTLNQCGEVENATKPF  
AALYVSQTAGWTGTRAGALQIPEAMOMAQYRENGIGTONVLYENOKOANOENKAIS  
QIVDRLTRLTSALGQDQVYPPNTLNQCGEVENATKPF  
LMSPOORAHGQVVELHVTYVPSQERNETTAAPICHEGKAYFPRGVFVNGTSNFIITO  
DLRGDISGINASVNVIQKEDRNLVEKAVNATLSDLOEGLKQEYIQKWAQVWLGIF  
GLIAUVMVTTLLCCMTSCSCLKGACSCSCKEDBDDSEPVLKGVKLYT"

卷三





GSAATVRLQAGNATEVPANSTVLSFCAAFDPKAYKDYLASGGDPITCYRMLCFT  
 TGTGQAATTTPEANMDDEFGGASCCLSYCHIDHPNKGCFDKLKGKVQVUPTCANIE  
 PUGVFTPLRNTVCTGMMDFKPFQGKCFKSSCDLRECHIPLKQFQKQFQKQFQKQFQ  
 TSTDVVRKAFTDINKEVKAQFKLTKNCRKFQKEDBGNLDSYFVKRHTMSNYQHNN  
 ETLYNLVNUKDCPAVAVHDFFKFRVDDPMVPSISROURKTYTMAWDLVYALRHFP  
 GIVLQVTLQDINGWYTFQDFVQAPGCVPVIDSYSLIMPILTRULRAESEHSH  
 LESTFVEPTSPGFLVRCFPLVRCFPLVRCFPLVRCFPLVRCFPLVRCFPLVRC  
 YAADPAMHAASGNLLDRKETCFSPVATLNVNAQFQTVKPGFNKDFDTFAVSGF  
 GSSVEKLHFFPAQDGNAASISDYDTRYNLPMTCDIRQLFVUVYDKFDCTDGGC  
 ANQVYNDVNDKSKVSGSISVYDQVYDQVYDQVYDQVYDQVYDQVYDQVYDQV  
 ISAKRNARTVAGVSICSTMRNROPHQKLKSIAATRGATVVTGTSKEYFQGWBNMLK  
 YSDMVEPHPLMGNDPKCDRAMPNMLRIMASLVLARKHNTCNLSHREAQV  
 REFLPLCCXCCYDQAVITSTSHKLVLSPNPYVNAQPGCDVTDYDOLYLGGM  
 NMQLHQBLTLYNRDVDFDVEFDAYLRKHFSMNTLSDDAVYCNSNYYAOGLV  
 KNFKAVALVQNNYEMSEACWCTEDLTGKGFHEPCSOHTMLVYQGDYDLYVLP  
 LGCAQYDUDLRTDLMERLARSLAIDPLTQYDQVYDQVYDQVYDQVYDQV  
 TGHMLDMYSVMLNTDNTSYWEPEPEYATMPTHQLVQAGCULCNQSLSRGACT  
 SEMMCGSLLYKPGFTGSSGDATAAYANWSUNIVQCQATANVNLSTDGNK  
 NLQHRLBLTLYNRDVDFDVEFDAYLRKHFSMNTLSDDAVYCNSNYYAOGLV  
 SPCLANCQVNGLYNCVGSNDTDFNATDWTNAGDYLTAECTLKUPAE  
 LRATLATEPLRSYLVATRVEPQDLSRBLHSLVNGKRPVPLVPLVPLVPL  
 GEYTFEGKGDYGDAVYRETTTYKLUNGDFEVLTSEHMPAAPTLYVQEHYVITGL  
 PTNISDEISVNTSYKQGMRSIIPARATVPLTQYDQVYDQVYDQVYDQV  
 AAVDALLCERALKYLPIKCSRIIPARATVPLTQYDQVYDQVYDQV  
 IVVYDELSMATHDLSVYNAHLRAXHYVWVGDPAQLPAPRPLTQKTEPEPEYEN  
 LMKJTGPMFLGRCRTPCAPIVOTVSLAIVDNLKLAHKDQSAQC  
 SAIYNRQPVQGIVRFLTRNPAWRKAFLSIPSYNQAVASV  
 VIFTQTTETAHSCVNVRENVATPAKIGLICMISORDLYDLOQTSLSI  
 AENVTPGLPDKCSKPLITQLEPTPLQYDQVYDQVYDQVYDQV  
 GPKRMQNYQGPMSKLTIREAIREVRAVGFDVESCHTRAVGTPNQ  
 LYAVPTGTVYDUTENNTETPYVNAKPPGQDFKHLIPLMYKGLPWNVYR  
 FGDSYDPRVVFHMLWFLGELTSYKQFVKG  
 APFLWAKRNPKVYPIKLNFLQNLDFHGHBAPSY  
 DMSVEPVPLIGDELRVNSACKVQHMAVKSALLADEPKV  
 SNLNLPGDGSLLYKNEPLQYDQVYDQVYDQVYDQV  
 YPLKLSATCITCRNLGGACWCHHANEYRQYLDAYNMIM  
 FTRLSLERNVAYAVNVQYDQVYDQVYDQVYDQV  
 BSYTQFOPYRKGQPLQYDQVYDQVYDQVYDQV  
 GSSKCKVCWSVLDLIDFVEWIKTSODISVSKV  
 KLUOSAQWQAPVYMLPQYDQVYDQVYDQVYDQV  
 DCATVHTANKWDLIISDMDPTRKTVKENDSKGEFTYLG  
 TEHSWNADYLKGMHFSWTAFTVNVNASSAEFLI  
 FORTNTPNLSPLSFDMSKPLKLRGTAVMSLKENQINOMYSLLEKGRLLTRENN  
 VVSSDILVNN"



GSSEVSLKIPPEAQDGDNALISDQYRRNLPMTMDIROLLEMEVNDVDCEDCYDGGCIN  
IANSQVNRNIDQSACFGPFWKGTMNRQPHQKLKSLAATGTVTGTGVTGCTV  
YSDVEUTPHLGWYHPKCBRAMPNMRLTANASLVLARKINTCCNLSHREYVRLAMECAQV.  
SMENSGGSVYRGGTSQSGDDETAVYANSVNFICQMAVFLAVNARVNSQVADLKVTR  
NLQBLRVECLYRGRDNEVDETTAVERLRKHFSQMLAVSILDAVYCNSYNAQCLV  
KNEFATVLYTONNVMSERAKCWTEDLTGSPHEFCSOFTMLVKQDDTVYLXPDPBRI  
LGAGCPVDDVLTQKGTLTMRSLYERPIVSLAIDAYPLTKHGPYQDADYFLTQYIQLKGADL  
RPFUCCCKCYDHVISTSTSKLVLSTNPYCNAPCDVDTYOTOLYLGMSYYCKSKHP1  
SLPCANGQGVLYKNTCTGSDNTDFRAIDCDTNGDYLANTCTERLKFAET  
LKATEPATFLKSYATGATVTPRSDRLELSWEVGPRKLNRYTQVTRVNSQVY  
GEYTFEGKGDGDAVYRGTYKLNGYFVULTSHTWMPMSLAPLTYOEHYVITGLY  
PTLNMSDESSANTYQNYQGMQYKSTLARVPCBPGTKSHAFGALYVPSRIVATC  
IIVVDEISWATNDLSVNAWRPAKHYTQIDCSRSTPLPARVECFVTCVNL  
LMKTGDPMLGTRCRPAEJUDTVALYDNTKLAQKDKSACQPMNHYKGTHDVS  
SANRNPQIGVYREPTRUPAWKAVFSPYNSQVAKSFLQPTDOSSEDY  
VIEFTOTTETAHSCVNVRNTRALTRAKISGLTMSDRDLYDKLOFTSLEIIPRNTVQ  
AEYNTGLFDCSKLTITGHPTQPHFSTKPLKXGKQHPLJLXKOMLSDT  
LVAUTPGYDVENTTEFRVNAKPLGTRDTRVATRNGYDVGCHTRDVA  
KGLSDRVUTVWLQWGFELTSMKPYFKVQGDRPTTSDYACMNSUC  
FDYVYNPFLDVOQHGFGNLQSHDQCQVHNRNAYASCDALIMTRCAVHBCFVVRV  
DWSTVBYPLGDELRVNSACRKYOMHVSALLADKFPTLHDIGNPKA1KQPAQEYEW  
KEYDPAQPCSDKA1KQPAQEYEWTFDPAKSAFTN1KQLPKQPSGHCQVSD1D  
SNLQDQGDSLTYKRAFHTPAFQDQVH1KQPAQEYEWTFDPAKSAFTN1KQLP  
YVPLKSACATCTRCNLLGAVCRHANEYROYLDAYNNMISAGRS1LWYKQFDTYLNNT  
FTRLOLUNAVANVNGKHFDFGRAGEVQH1KQPAQEYEWTFDPAKSAFTN1KQLP  
AFLBWKANRKP1K1LNQHDIANTVYDTRKPAHGDV1GTCVQD1KQLP  
TBSACASST1YTFDGRVEGQDYLFRNARQCVL1TGSVYGLTPSKGPQAQSINGVTLIG  
ESVKTQFNTYFKRQD1IQLQPEVTFQDQDLEPQSRTDQFELBLLDFT1QRYK  
EGATYQHFTYQDHSQHGLLGMGLAKRSQSPKLEDFPTMDSTVTKP1T1DACT  
GSMSICVCVS1D1LJDDFEL1IKSDOLSLVSKVYKUTDIA1SFMLWCKGQHIVETYP  
KLOSAQWAQDQVAMPN1KQMRNLLKCDLQVNGENAW1PKGMVANVAKYQOLQYIN  
TLTLVATVQYRNRTHFGSDQRMV1QDQVY1QDQVY1QDQVY1QDQVY1QDQVY1  
DCATVTHANKWDL1I1SDWYDPRKTHVNTC1DSEKFGF1PFLQCCP1KORLALG5JAYUK  
STWSNMD1WYKLUSS1SATUTVNTNSSEASPE1LQGAVLQSKPCKQDQGRTMHNRY  
FWRATNP1QUSSTYLSFDNSKFPLKLQGRTAVMS1KENQDMSL1RREY1RREY1



Query Match	90.9%	Score 20;	DB 14;	Length 29573;		COMMENT	On or before Jan 5, 2004 this sequence version replaced gi:32454355, gi:32454356, gi:32454357, gi:32454358.
Best Local Similarity	75.0%;	Pred. No.	0.013;	Indels	0;	FEATURES	Location/Qualifiers
Matches	15;	Conservative	5;	Mismatches	0;	source	1. .29592
Qy	1 GUGAACUCAUCUGAGGCU 20   :    :    :    :    :    :    Db 707 GTGAACTACTCGTAGTC 726	SARS coronavirus	Sin846	29577 bp	RNA	linear	/organism="SARS coronavirus Shanghai QXC1"
RESULT 14							
LOCUS	AY559094	AY559094	29577 bp	RNA	linear	VRL 24-SEP-2004	
DEFINITION	SARS coronavirus	Sin846	complete genome.				
VERSION	AY559094	AY559094	GI:45645021				
KEYWORDS	SARS coronavirus	Sin846					
ORGANISM	SARS coronavirus	Sin846					
VIRUSES:	sRNA positive-strand viruses, no DNA stage; Nidovirales;						
Coronaviridae: Coronaviruses.							
1 (bases 1 to 29577)						CDS	
REFERENCE							
AUTHORS	Vega, V.B., Ruan, Y., Liu, J., Lee, W.H., Wei, C.L., Se Thoe, S.Y., Tang, K.F., Zhang, T., Lin, S., Kolathar, P.R., Ooi, E.E., Ling, A.E., Stanton, L.W., Long, P.M. and Liu, B.T.						
TITLE	Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003 (er)	BMC Infect. Dis.	4 (1), 32 (2004)				
JOURNAL							
PUBLMED	15347439	2 (bases 1 to 29577)					
AUTHORS	Vega, V.B., Ruan, Y., Liu, J., Lee, W.H., Wei, C.L., Se Thoe, S.Y., Tang, K.F., Zhang, T., Lin, S., Kolathar, P.R., Ooi, E.E., Ling, A.E., Stanton, L.W., Long, P.M. and Liu, B.T.						
Direct Submission							
JOURNAL	Submitted (24-FEB-2004)	Genome Institute of Singapore	Street #02-01, Genome Institute of Singapore, 60, Biopolis Street #1386782, Singapore				
FEATURES	source						
ORIGIN							
Query Match	90.9%	Score 20;	DB 14;	Length 29577;			
Best Local Similarity	75.0%;	Pred. No.	0.013;	Indels	0;	Gaps	
Matches	15;	Conservative	5;	Mismatches	0;		
Qy	1 GUGAACUCAUCUGAGGCU 20   :    :    :    :    :    :    :    :    :    :    Db 760 GTGAACTACTCGTAGTC 779	SARS coronavirus	Shanghai QXC1	29592 bp	RNA	linear	VRL 05-JAN-2004
RESULT 15							
LOCUS	AY63059	AY63059	29592 bp	RNA	linear	VRL 05-JAN-2004	
DEFINITION	SARS coronavirus	Shanghai QXC1	complete genome.				
ACCESSION	AY63059	AY63059	GI:40457433				
VERSION							
KEYWORDS							
SOURCE							
ORGANISM	SARS coronavirus	Shanghai QXC1					
VIRUSES:	sRNA positive-strand viruses, no DNA stage; Nidovirales;						
Coronaviridae: Coronaviruses.							
1 (bases 1 to 29592)							
AUTHORS	Xuan, Z., Zhang, X., Hu, Y., Lan, S., Zhou, Z., Wang, H. and Wen, Y.						
TITLE	Analysis of SARS coronavirus genome in Shanghai isolates						
JOURNAL	Unpublished						
REFERENCE							
AUTHORS	Xuan, Z., Zhang, X., Hu, Y., Lan, S., Zhou, Z., Wang, H. and Wen, Y.						
TITLE	Direct Submission						
JOURNAL	Submitted (11-NOV-2003)	Key Lab of Medical Molecular Virology, Shanghai Medical College, Fudan University, 138 Yi Yuan Road, Shanghai 200032, P.R. China					



1. .29645  
     /organism="SARS coronavirus GZ-C"  
     /mol type="genomic RNA"  
     /isolate="GZ-C"  
     /db\_xref="taxon:249064"

ORIGIN

Query Match    90.9%;    Score 20;    DB 14;    Length 29620;  
     Best Local Similarity 75.0%;    Pred. No. 0.013;  
     Matches 15;    Conservative 5;    Mismatches 0;    Indels 0;    Gaps 0;

Qy            1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:|:|:  
         Db      729 GTGAACTCACTCGTGAAGTC 748

RESULT 17

AY94978        1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:|:  
         LOCUS    SARS coronavirus GZ-B, complete genome.  
         VERSION AY394978  
         DEFINITION SARS coronavirus GZ-B, complete genome.  
         ACCESION AY394978.1  
         KEYWORD SOURCE  
         ORGANISM SARS coronavirus GZ-B  
               Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
               Coronaviridae; Coronavirus.  
         1 (bases 1 to 29640)

REFERENCE AUTHORS  
     CONSRMT The SARS epidemiology consortium of Guangdong  
     TITLE From independent foci of epidemic outbreak to large genomic  
     JOURNAL Alteration in late phase viruses: evolution of the SARS-coronavirus  
     FEATURES Unpublished  
     2 (bases 1 to 29640)

REFERENCE AUTHORS  
     CONSRMT The SARS epidemiology consortium of Guangdong  
     TITLE Direct Submission  
     JOURNAL Submitted (19-SEP-2003) Guangdong, China  
     FEATURES Location/Qualifiers  
     1. 29640  
         /organism="SARS coronavirus GZ-B"  
         /mol type="genomic RNA"  
         /isolate="GZ-B"  
         /db\_xref="taxon:249063"

ORIGIN

Query Match    90.9%;    Score 20;    DB 14;    Length 29640;  
     Best Local Similarity 75.0%;    Pred. No. 0.013;  
     Matches 15;    Conservative 5;    Mismatches 0;    Indels 0;    Gaps 0;

Qy            1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:|:  
         Db      704 GTGAACTCACTCGTGAAGTC 723

RESULT 18

AY94979        1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:  
         LOCUS    SARS coronavirus GZ-C, complete genome.  
         VERSION AY394979  
         DEFINITION ACCESION  
         ACCESION AY394979  
         KEYWORD SOURCE  
         ORGANISM SARS coronavirus GZ-C  
               Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
               Coronaviridae; Coronavirus.  
         1 (bases 1 to 29645)

REFERENCE AUTHORS  
     CONSRMT The SARS epidemiology consortium of Guangdong  
     TITLE From independent foci of epidemic outbreak to large genomic  
     JOURNAL Alteration in late phase viruses: evolution of the SARS-coronavirus  
     FEATURES Unpublished  
     2 (bases 1 to 29645)

ORIGIN

Query Match    90.9%;    Score 20;    DB 14;    Length 29645;  
     Best Local Similarity 75.0%;    Pred. No. 0.013;  
     Matches 15;    Conservative 5;    Mismatches 0;    Indels 0;    Gaps 0;

Qy            1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:  
         Db      724 GTGAACTCACTCGTGAAGTC 743

RESULT 19

AY394982        1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:  
         LOCUS    SARS coronavirus HGZ8L1-B, partial genome.  
         VERSION AY394982  
         DEFINITION SARS coronavirus HGZ8L1-B  
         KEYWORD SOURCE  
         ORGANISM SARS coronavirus HGZ8L1-B  
               SARS coronavirus HGZ8L1-B  
               Viruses; ssRNA Positive-strand viruses, no DNA stage; Nidovirales;  
               Coronaviridae; Coronavirus.  
         1 (bases 1 to 29646)

REFERENCE AUTHORS  
     CONSRMT The SARS epidemiology consortium of Guangdong  
     TITLE From independent foci of epidemic outbreak to large genomic  
     JOURNAL Alteration in late phase viruses: evolution of the SARS-coronavirus  
     FEATURES Unpublished  
     2 (bases 1 to 29646)

ORIGIN

Query Match    90.9%;    Score 20;    DB 14;    Length 29646;  
     Best Local Similarity 75.0%;    Pred. No. 0.013;  
     Matches 15;    Conservative 5;    Mismatches 0;    Indels 0;    Gaps 0;

Qy            1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:  
         Db      724 GTGAACTCACTCGTGAAGTC 743

RESULT 20

AY395003        1 GUGAACUCACUCGGAGGCUC 20  
               |:|:|||:|:|:|:  
         LOCUS    SARS coronavirus ZS-C, complete genome.  
         VERSION AY395003  
         DEFINITION SARS coronavirus ZS-C  
         KEYWORD SOURCE  
         ORGANISM SARS coronavirus ZS-C  
               Viruses; ssRNA Positive-strand viruses, no DNA stage; Nidovirales;  
               Coronaviridae; Coronavirus.  
         1 (bases 1 to 29647)

REFERENCE AUTHORS  
     CONSRMT The SARS epidemiology consortium of Guangdong  
     TITLE From independent foci of epidemic outbreak to large genomic  
     JOURNAL Alteration in late phase viruses: evolution of the SARS-coronavirus  
     FEATURES Unpublished  
     2 (bases 1 to 29647)

AUTHORS	The SARS epidemiology consortium of Guangdong	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
CONTRIB	Direct Submission	REFERENCE 1 (bases 1 to 29665)
JOURNAL	Submitted (19-SEP-2003) Guangdong	AUTHORS The SARS epidemiology consortium of Guangdong
FEATURES	Location/Qualifiers 1 .29647 /organism="SARS coronavirus ZS-C" /mol_type="genomic RNA" /isolate="ZS-C" /db_xref="taxon:249088"	CONSITM From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus
SOURCE		JOURNAL Unpublished 2 (bases 1 to 29665)
ORIGIN		REFERENCE 2 (bases 1 to 29665)
RESULT 21	Query Match 90.9%; Score 20; DB 14; Length 29647;	AUTHORS The SARS epidemiology consortium of Guangdong
AV59086	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	CONSITM Direct Submission
LOCUS 29661 bp RNA	Matches 15; Conservative 5; Mismatches 0;	TITLE Submitted (19-SEP-2003) Guangdong, China
DEFINITION SARS coronavirus Sin849, complete genome.	FEATURES Location/Qualifiers 1 .29665	JOURNAL Location/Qualifiers
ACCESSION AY59086		ORGANISM /organism="SARS coronavirus JMD" /mol_type="genomic RNA" /isolate="JMD" /db_xref="taxon:249073"
VERSION AY59086.1		ORIGIN
KEYWORDS	1 GUGAACUCUCCUGAGUC 20	Query Match 90.9%; Score 20; DB 14; Length 29665;
SOURCE	Db 725 GTGAACTCTACTCGTGTGCTC 744	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;
ORGANISM	SARS coronavirus Sin849	FEATURES source
RESULT 22	Query Match 90.9%; Score 20; DB 14; Length 29661;	Query Match 90.9%; Score 20; DB 14; Length 29670;
AV394988	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;
LOCUS 29665 bp RNA	Matches 15; Conservative 5; Mismatches 0;	DEFINITION 1 .29670
DEFINITION SARS coronavirus JMD, partial genome.	FEATURES source	AUTHORS The SARS epidemiology consortium of Guangdong
ACCESSION AY394988		CONSITM From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus
VERSION AY394988.1		JOURNAL Unpublished 2 (bases 1 to 29670)
KEYWORDS	1 GUGAACUCUCCUGAGUC 20	REFERENCE 2 (bases 1 to 29670)
SOURCE	Db 760 GTGAACTCTACTCGTGTGCTC 779	AUTHORS Vega,V.B., Ruan,Y., Liu,J., Lee,W.H., Wei,C.L., Se Thoe,S.Y., Tang,K.F., Zhang,T., Lin,S., Kollarikar,P.R., Ooi,E.E., Ee,L.A., Stanton,L.W., Long,P.M. and Liu,E.T.
ORGANISM	SARS coronavirus Sin849	TITLE Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003
RESULT 23	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	JOURNAL Stanton,L.W., Long,P.M. and Liu,E.T.
AY59082	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	DEFINITION 1 .29670 bp RNA linear VRL 24-SEP-2004
LOCUS 29670 bp RNA	Matches 15; Conservative 5; Mismatches 0;	ACCESSION AY59082
DEFINITION SARS coronavirus Sin852, complete genome.	FEATURES source	VERSION AY59082.1 GI:45644996
ACCESSION AY59082		KEYWORDS
VERSION AY59082.1		SOURCE SARS coronavirus Sin852
KEYWORDS		ORGANISM SARS coronavirus Sin852
SOURCE		Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
ORGANISM	SARS coronavirus Sin849	REFERENCE 1 (bases 1 to 29670)
RESULT 24	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	AUTHORS Vega,V.B., Ruan,Y., Liu,J., Lee,W.H., Wei,C.L., Se Thoe,S.Y., Tang,K.F., Zhang,T., Lin,S., Kollarikar,P.R., Ooi,E.E., Ee,L.A., Stanton,L.W., Long,P.M. and Liu,E.T.
AY59082	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	TITLE Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003
LOCUS 29670 bp RNA	Matches 15; Conservative 5; Mismatches 0;	JOURNAL Stanton,L.W., Long,P.M. and Liu,E.T.
DEFINITION SARS coronavirus Sin852, complete genome.	DEFINITION 1 .29670	DEFINITION 1 .29670
ACCESSION AY59082		ACCESSION AY59082
VERSION AY59082.1		VERSION AY59082.1 GI:45644996
KEYWORDS		KEYWORDS
SOURCE		SOURCE SARS coronavirus Sin852
ORGANISM	SARS coronavirus Sin849	ORGANISM SARS coronavirus Sin852
RESULT 25	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	VIRUSES
AY394749	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	DEFINITION 1 .29670 bp RNA linear VRL 24-SEP-2004
LOCUS 29661 bp RNA	Matches 15; Conservative 5; Mismatches 0;	ACCESSION AY394749
DEFINITION SARS coronavirus Sin852, complete genome.	FEATURES source	VERSION AY394749
ACCESSION AY394749		KEYWORDS
VERSION AY394749.1		SOURCE SARS coronavirus Sin852
KEYWORDS		ORGANISM SARS coronavirus Sin852
SOURCE		VIRUSES
ORGANISM	SARS coronavirus Sin849	DEFINITION 1 .29670 bp RNA linear VRL 24-SEP-2004
RESULT 26	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	ACCESSION AY394749
AY394749	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	VERSION AY394749
LOCUS 29661 bp RNA	Matches 15; Conservative 5; Mismatches 0;	KEYWORDS
DEFINITION SARS coronavirus Sin852, complete genome.	DEFINITION 1 .29670	SOURCE SARS coronavirus Sin852
ACCESSION AY394749		ORGANISM SARS coronavirus Sin852
VERSION AY394749.1		VIRUSES
KEYWORDS		DEFINITION 1 .29670
SOURCE		ACCESSION AY394749
ORGANISM	SARS coronavirus Sin849	VERSION AY394749
RESULT 27	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	VERSION AY394749
AY394749	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	KEYWORDS
LOCUS 29661 bp RNA	Matches 15; Conservative 5; Mismatches 0;	SOURCE SARS coronavirus Sin852
DEFINITION SARS coronavirus Sin852, complete genome.	DEFINITION 1 .29670	ORGANISM SARS coronavirus Sin852
ACCESSION AY394749		VIRUSES
VERSION AY394749.1		DEFINITION 1 .29670
KEYWORDS		ACCESSION AY394749
SOURCE		VERSION AY394749
ORGANISM	SARS coronavirus Sin849	KEYWORDS
RESULT 28	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	SOURCE SARS coronavirus Sin852
AY394749	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	DEFINITION 1 .29670
LOCUS 29661 bp RNA	Matches 15; Conservative 5; Mismatches 0;	ACCESSION AY394749
DEFINITION SARS coronavirus Sin852, complete genome.	FEATURES source	VERSION AY394749
ACCESSION AY394749		KEYWORDS
VERSION AY394749.1		SOURCE SARS coronavirus Sin852
KEYWORDS		ORGANISM SARS coronavirus Sin852
SOURCE		VIRUSES
ORGANISM	SARS coronavirus Sin849	DEFINITION 1 .29670
RESULT 29	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	ACCESSION AY394749
AY394749	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	VERSION AY394749
LOCUS 29661 bp RNA	Matches 15; Conservative 5; Mismatches 0;	KEYWORDS
DEFINITION SARS coronavirus Sin852, complete genome.	DEFINITION 1 .29670	SOURCE SARS coronavirus Sin852
ACCESSION AY394749		ORGANISM SARS coronavirus Sin852
VERSION AY394749.1		VIRUSES
KEYWORDS		DEFINITION 1 .29670
SOURCE		ACCESSION AY394749
ORGANISM	SARS coronavirus Sin849	VERSION AY394749
RESULT 30	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	KEYWORDS
AY394749	Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;	SOURCE SARS coronavirus Sin852
LOCUS 29661 bp RNA	Matches 15; Conservative 5; Mismatches 0;	DEFINITION 1 .29670
DEFINITION SARS coronavirus Sin852, complete genome.	DEFINITION 1 .29670	ACCESSION AY394749
ACCESSION AY394749		VERSION AY394749
VERSION AY394749.1		KEYWORDS
KEYWORDS		SOURCE SARS coronavirus Sin852
SOURCE		ORGANISM SARS coronavirus Sin852
ORGANISM	SARS coronavirus JMD	VIRUSES

RESULT 24  
AY394996 AY394996 29683 bp RNA linear VRL 29-JAN-2004

LOCUS SARS coronavirus ZS-B, complete genome.

DEFINITION SARS coronavirus ZS-B, complete genome.

VERSION AY394996

KEYWORDS SARS coronavirus ZS-B

ORGANISM SARS coronavirus ZS-B

SOURCES Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 29683)

REFERENCE

AUTHORS The SARS epidemiology consortium of Guangdong

CONSRNM From independent foci of epidemic outbreak to large genomic

TITLE alteration in late phase viruses: evolution of the SARS-coronavirus

JOURNAL Unpublished

FEATURES 2 (bases 1 to 29683)

REFERENCE

AUTHORS The SARS epidemiology consortium of Guangdong

CONSRNM Direct Submission

TITLE Submitted (19-SEP-2003) Guangdong, China

JOURNAL Location/Qualifiers

FEATURES 1 . 29683 /organism="SARS coronavirus ZS-B"  
/mol\_type="genomic RNA"  
/isolate="ZS-B"  
/db\_xref="taxon:249081"

ORIGIN

Query Match 90.9%; Score 20; DB 14; Length 29683;  
Best Local Similarity 75.0%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Db 761 GTGAACTACTCGTGTAGTC 780

RESULT 25  
AY394997 AY394997 29683 bp RNA linear VRL 29-JAN-2004

LOCUS SARS coronavirus ZS-A, complete genome.

DEFINITION SARS coronavirus ZS-A

VERSION AY394997

KEYWORDS SARS coronavirus ZS-A

ORGANISM SARS coronavirus ZS-A

SOURCES Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 29683)

REFERENCE

AUTHORS The SARS epidemiology consortium of Guangdong

CONSRNM From independent foci of epidemic outbreak to large genomic

TITLE alteration in late phase viruses: evolution of the SARS-coronavirus

JOURNAL Unpublished

FEATURES 2 (bases 1 to 29683)

REFERENCE

AUTHORS The SARS epidemiology consortium of Guangdong

CONSRNM Direct Submission

TITLE Submitted (19-SEP-2003) Guangdong, China

JOURNAL Location/Qualifiers

FEATURES 1 . 29683 /organism="SARS coronavirus ZS-A"  
/mol\_type="genomic RNA"  
/isolate="ZS-A"  
/db\_xref="taxon:249082"

ORIGIN

Query Match 90.9%; Score 20; DB 14; Length 29683;  
Best Local Similarity 75.0%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Db 724 GTGAACTACTCGTGTAGTC 743

RESULT 26  
AY394983 AY394983 29639 bp RNA linear VRL 29-JAN-2004

LOCUS SARS coronavirus HSZ2-A, complete genome.

DEFINITION SARS coronavirus HSZ2-A

VERSION AY394983

KEYWORDS SARS coronavirus HSZ2-A

ORGANISM SARS coronavirus HSZ2-A

SOURCES Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 29699)

REFERENCE

AUTHORS The SARS epidemiology consortium of Guangdong

CONSRNM From independent foci of epidemic outbreak to large genomic

TITLE alteration in late phase viruses: evolution of the SARS-coronavirus

JOURNAL Unpublished

FEATURES 2 (bases 1 to 29699)

REFERENCE

AUTHORS The SARS epidemiology consortium of Guangdong

CONSRNM Direct Submission

TITLE Submitted (19-SEP-2003) Guangdong, China

JOURNAL Location/Qualifiers

FEATURES 1 . 29699 /organism="SARS coronavirus HSZ2-A"  
/mol\_type="genomic RNA"  
/isolate="HSZ2-A"  
/db\_xref="taxon:249068"

ORIGIN

Query Match 90.9%; Score 20; DB 14; Length 29699;  
Best Local Similarity 75.0%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Db 724 GTGAACTACTCGTGTAGTC 743

RESULT 27  
AY283795 AY283795 29705 bp RNA linear VRL 12-AUG-2003

LOCUS SARS coronavirus sin2677, complete genome.

DEFINITION SARS coronavirus sin2677

VERSION AY283795

KEYWORDS SARS coronavirus Sin2677

ORGANISM SARS coronavirus Sin2677

SOURCES Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 29705)

REFERENCE

AUTHORS Chia, J.-M., Ng, P., Chiu, K.P., Lim, L., Zhang, T., Chan, K.P., Oon, L.E.L., Ng, M.L., Leo, S.Y., Ng, L.F.P., Ren, E.C., Stanton, L.W., Long, P.M. and Liu, E.T.

CONSRNM Comparative full-length genome sequence analysis of 14 SARS

TITLE coronaviruses isolates and common mutations associated with putative

JOURNAL origins of infection

FEATURES Lancet 361 (9371), 1779-1785 (2003)

ORIGIN

Query Match 90.9%; Score 20; DB 14; Length 29683;  
Best Local Similarity 75.0%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Db 724 GTGAACTACTCGTGTAGTC 743

RESULT 28  
AY283795 AY283795 29705 bp RNA linear VRL 12-AUG-2003

LOCUS SARS coronavirus sin2677, complete genome.

DEFINITION SARS coronavirus sin2677

VERSION AY283795

KEYWORDS SARS coronavirus Sin2677

ORGANISM SARS coronavirus Sin2677

SOURCES Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 29705)

REFERENCE

AUTHORS Chia, J.-M., Ng, P., Chiu, K.P., Lim, L., Zhang, T., Chan, K.P., Oon, L.E.L., Ng, M.L., Leo, S.Y., Ng, L.F.P., Ren, E.C., Stanton, L.W., Long, P.M. and Liu, E.T.

CONSRNM Comparative full-length genome sequence analysis of 14 SARS

TITLE coronaviruses isolates and common mutations associated with putative

JOURNAL origins of infection

FEATURES Lancet 361 (9371), 1779-1785 (2003)

ORIGIN

Query Match 90.9%; Score 20; DB 14; Length 29683;  
Best Local Similarity 75.0%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Db 724 GTGAACTACTCGTGTAGTC 743

RESULT 29  
AY283795 AY283795 29705 bp RNA linear VRL 12-AUG-2003

LOCUS SARS coronavirus sin2677, complete genome.

DEFINITION SARS coronavirus sin2677

VERSION AY283795

KEYWORDS SARS coronavirus Sin2677

ORGANISM SARS coronavirus Sin2677

SOURCES Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 29705)

REFERENCE

AUTHORS Wei, C.L., Ling, A.E., Vega, Y.B., Thoreau, H., Se Thoe, S.Y., Lambert, E., Zhang, T., Wong, M., Se Thoe, S.Y., Chan, K.P. and Ruan, Y.

CONSRNM Direct Submission

TITLE Submitted (27-APR-2003) Genome Institute of Singapore, 1 Science Park Road, The Capricorn #05-01, Singapore 117528, Singapore

JOURNAL

FEATURES	Location/Qualifiers		TITLE	Long, P.M. and Liu, E.T.
source	1 .29/05 "SARS coronavirus Sin2677" /virion /mol type="genomic RNA" /isolate="SIN2677" /db_xref="taxon:235413" /country="Singapore"			Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection
ORIGIN			JOURNAL	Lancet 361 (9371), 1779-1785 (2003)
	Query Match 90.9%; Score 20; DB 14; Length 29705; Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;		MEDLINE	22667074
Matches 15; Conservative 5; Mismatches 0;			PUBMED	12781537
Qy 1 GUGAACUCACUCUGGAGCTC 20			REMARK	Erratum in: Lancet. 2003 May 24;361(9371):1832.
Db 760 GTGAACTCACTCGTGAAGTC 779			REFERENCE	2 (bases 1 to 29706)
			AUTHORS	Wei,C.L., Thoreau,H., Chia,J.-M., Chiu,K.P., Ng,P., Lim,L., Lambert,E., Zhang,T., Wong,M., Se Thoe,S.Y., Chan,K.P. and Ruan,Y.
			TITLE	Direct Submission (27-APR-2003) Genome Institute of Singapore, 1 Science Park Road, The Capricorn #05-01, Singapore 117528, Singapore
			JOURNAL	
			FEATURES	Location/Qualifiers
			source	1 . 29706 /organism="SARS coronavirus Sin2748" /virus /country="Singapore"
RESULT 28			ORIGIN	
AV394980	AY394980 29705 bp RNA linear VRL 29-JAN-2004		Query Match	90.9%; Score 20; DB 14; Length 29706;
LOCUS	AY394980		Best Local Similarity	75.0%; Pred. No. 0.013;
DEFINITION	SARS coronavirus GZ-D, partial genome.		Matches	5; Mismatches 0; Indels 0; Gaps 0;
VERSION	AY394980.1		DEFINITION	
ACCESSION	GI:37624323		Match	
KEYWORDS			Conservative	
SOURCE	SARS coronavirus GZ-D		Accession	
ORGANISM	SARS coronavirus GZ-D Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronaviruses.		AY394987	AY394987 SARS coronavirus H2S2-Fb, complete genome.
REFERENCE	1 (bases 1 to 29705)		VERSION	AY394987 SARS coronavirus H2S2-Fb
CONTRSM	The SARS epidemiology consortium of Guangdong		KEYWORDS	AY394987.1 GI:37624330
TITLE	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus		SOURCE	SARS coronavirus H2S2-Fb
JOURNAL	Unpublished		ORGANISM	SARS coronavirus H2S2-Fb viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronaviruses.
REFERENCE	2 (bases 1 to 29705)		REFERENCE	1 (bases 1 to 29709)
CONTRSM	The SARS epidemiology consortium of Guangdong		AUTHORS	The SARS epidemiology consortium of Guangdong
TITLE	Direct Submission (19-SEP-2003) Guangdong, China		CONTRSM	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus
JOURNAL	Submitted (19-SEP-2003) Guangdong, China		TITLE	
FEATURES	1 .29705		JOURNAL	Unpublished
source	/organism="SARS coronavirus GZ-D" /mol type="genomic RNA" /isolate="GZ-D" /db_xref="taxon:249065"		FEATURES	2 (bases 1 to 29709)
ORIGIN			REFERENCE	AUTHORS
	Query Match 90.9%; Score 20; DB 14; Length 29705; Best Local Similarity 75.0%; Pred. No. 0.013; Indels 0; Gaps 0;		CONTRSM	The SARS epidemiology consortium of Guangdong
Matches 15; Conservative 5; Mismatches 0;			TITLE	Direct Submission (19-SEP-2003) Guangdong, China
Qy 1 GUGAACUCACUCUGGAGCTC 20			JOURNAL	Submitted (19-SEP-2003) Guangdong, China
Db 730 GTGAACTCACTCGTGAAGTC 749			FEATURES	Location/Qualifiers
			source	1 . 29709 /organism="SARS coronavirus H2S2-Fb" /mol type="genomic RNA" /isolate="H2S2-Fb" /db_xref="taxon:249072"
RESULT 29			ORIGIN	
AY283797	AY283797 29706 bp RNA linear VRL 12-AUG-2003		Query Match	90.9%; Score 20; DB 14; Length 29709;
LOCUS	SARS coronavirus Sin2748, complete genome.		Best Local Similarity	75.0%; Pred. No. 0.013;
DEFINITION	AY283797		Matches	5; Mismatches 0; Indels 0; Gaps 0;
VERSION	GI:30468045		DEFINITION	
ACCESSION	AY283797.1		Match	
KEYWORDS	SARS coronavirus Sin2748		Conservative	
SOURCE	SARS coronavirus Sin2748		Accession	
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronaviruses.		AY	1 GUGAACUCACUCUGGAGCTC 20
REFERENCE	1 (bases 1 to 29706)		VERSION	734 GTGAACTCACTCGTGAAGTC 753
AUTHORS	Chia,J.-M., Ng,P., Chiu,K.P., Lim,L., Zhang,T., Thoreau,H., Se Thoe,S.Y., Ruan,Y., Wei,C.L., Ling,A.E., Vega,V.B., Thoreau,H., Se Thoe,S.Y., Chia,J.-M., Ng,M.L., Leo,S.Y., Ng,L.F.P., Ren,E.C., Stanton,L.W., Oon,L.E.L., Ng,M.L., Leo,S.Y., Ng,L.F.P., Ren,E.C., Stanton,L.W.,		JOURNAL	
			FEATURES	
			REFERENCE	Search completed: July 21, 2005, 00:02:38

Fri Jul 22 12:38:06 2005

us-10-848-737-1.oli.rge

Page 19

Job time : 1700 secs

THIS PAGE IS BLANK